

Genotex version 4.5
Copyright (c) 1992 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:55:49 ; Search time 13.05 seconds
(without alignments)
475,410 Million cell updates/sec

Title: US-09-788-626-2

Perfect score: 1147

Sequence: 1 THICKVAKLFFRRKRENYR ... IGLHPSYIAVIRAKLIMD 254

Scoring table: BLOSUM62

Gapop: 10.0 ; Gapext: 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued: Patents-AA*

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*

3: /cgn2_6/prodata/2/1aa/6A_COMB.pep.*

4: /cgn2_6/prodata/2/1aa/6B_COMB.pep.*

5: /cgn2_6/prodata/2/1aa/PTMS_COMB.pep.*

6: /cgn2_6/prodata/2/1aa/backfill1.pep.*

7: /cgn2_6/prodata/2/1aa/backfill2.pep.*

8: /cgn2_6/prodata/2/1aa/backfill3.pep.*

9: /cgn2_6/prodata/2/1aa/backfill4.pep.*

10: /cgn2_6/prodata/2/1aa/backfill5.pep.*

11: /cgn2_6/prodata/2/1aa/backfill6.pep.*

12: /cgn2_6/prodata/2/1aa/backfill7.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	99.2	320	US-08-964-308-2	Sequence 2, Appl 1
2	1336	99.2	320	US-08-964-313-2	Sequence 2, Appl 1
3	1336	99.2	320	US-09-069-138-2	Sequence 2, Appl 1
4	1336	99.2	385	US-08-036-210-5	Sequence 5, Appl 1
5	1336	99.2	385	US-08-449-609-5	Sequence 5, Appl 1
6	1314.5	97.6	322	US-08-964-308-8	Sequence 8, Appl 1
7	1314.5	97.6	322	US-08-964-313-8	Sequence 8, Appl 1
8	1314.5	97.6	322	US-09-069-138-8	Sequence 1, Appl 1
9	1060	78.7	196	US-08-685-992-1	Sequence 1, Appl 1
10	1060	78.7	196	US-09-144-925-1	Sequence 1, Appl 1
11	811	60.2	134	US-08-685-992-2	Sequence 2, Appl 1
12	811	60.2	134	US-09-144-925-2	Sequence 2, Appl 1
13	508.5	37.0	278	US-08-444-345-27	Sequence 17, Appl 1
14	508.5	37.0	278	US-08-201-697-16	Sequence 17, Appl 1
15	498.5	37.0	254	US-08-685-992-14	Sequence 14, Appl 1
16	498.5	37.0	254	US-09-144-925-14	Sequence 14, Appl 1
17	490	36.4	273	US-08-201-697-17	Sequence 17, Appl 1
18	484.5	35.0	251	US-08-685-992-15	Sequence 15, Appl 1
19	484.5	35.0	251	US-09-144-925-15	Sequence 15, Appl 1
20	481	35.7	257	US-08-685-992-6	Sequence 6, Appl 1
21	481	35.7	257	US-09-144-925-6	Sequence 6, Appl 1
22	478.5	35.5	266	US-08-685-992-12	Sequence 12, Appl 1
23	478.5	35.5	266	US-09-144-925-12	Sequence 12, Appl 1
24	474	35.2	137	US-08-685-992-5	Sequence 2, Appl 1
25	474	35.2	137	US-09-144-925-5	Sequence 2, Appl 1
26	473.5	35.2	263	US-08-685-992-5	Sequence 5, Appl 1
27	473.5	35.2	263	US-09-144-925-5	Sequence 5, Appl 1

28	471.5	35.0	1501	2	US-08-447-464-3	Sequence 3, Appl 1
29	471.5	35.0	1501	2	US-08-716-679-3	Sequence 3, Appl 1
30	469	34.8	258	2	US-08-685-992-19	Sequence 19, Appl 1
31	469	34.8	258	2	US-09-144-925-19	Sequence 19, Appl 1
32	468.5	34.8	593	1	US-08-202-389-12	Sequence 12, Appl 1
33	468.5	34.6	250	2	US-08-685-992-7	Sequence 7, Appl 1
34	466.5	34.0	250	2	US-09-144-925-7	Sequence 7, Appl 1
35	464.5	34.5	1445	1	US-08-446-986A-2	Sequence 2, Appl 1
36	464.5	34.5	1445	1	US-08-446-986A-2	Sequence 2, Appl 1
37	464.5	34.5	1911	1	US-08-348-006B-5	Sequence 5, Appl 1
38	464.5	34.5	1911	2	US-08-800-825A-5	Sequence 5, Appl 1
39	464.5	34.5	1911	4	US-09-158-657-5	Sequence 5, Appl 1
40	464.5	34.5	1911	5	PCT-US94-10166-5	Sequence 5, Appl 1
41	463.5	34.4	593	1	US-08-018-129-5	Sequence 5, Appl 1
42	463.5	34.4	593	2	US-08-448-986A-3	Sequence 3, Appl 1
43	461.5	34.3	1442	1	US-08-015-986A-3	Sequence 3, Appl 1
44	461.5	34.3	1442	2	US-08-446-986A-3	Sequence 3, Appl 1
45	460	34.1	1188	1	US-08-201-697-4	Sequence 4, Appl 1

ALIGNMENTS

RESULT 1
US-08-964-308-2
Sequence 2, Application US/08964308
Patent No. 6066715
GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: PRIEST, RICHARD
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: ROBERT J. NORTH - MERCK & CO., INC.,
SHELBY, 124 EAST LINTON AVENUE - P.O. BOX 2000
CITY: RAMWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,308
FILING DATE: 04-Nov-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 19840 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594,7262
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-308-2
Query Match 99.2% Score 1336; DB 3; Length 320;
Best Local Similarity 99.2% Pred No. 8 3e-135;
Matches 254; Gaps 0; InDels 2; Gaps 1;
UY 1 DPCGVAKLPKNNRRYNDVSPDHSRIKLQHDNDYINASLIMKRIKORSYITLQGM 60

Query Match 99.2% Score 1336; DB 4; Length 320.
Best Local Similarity 99.2% Pred. No. 8.3e-135;
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DEPRVAKLPKNNRNPNRYSPFTHSRKIKLHEDNDYINASLTKMEFAORSYITLGGPL 60
DB 23 DEPRVAKLPKNNRNPNRYSPFTHSRKIKLHEDNDYINASLTKMEFAORSYITLGGPL 88
QY 61 PNTGHEWEMWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 120
DB 89 PNTGHEWEMWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 148
QY 121 IKSYTV--TELENLTTOETREILHEHYTTWPPGVPSPASFLNLFKVRSGSLSPH 178
DB 149 IKSYTVQLLENLITJQETREILHEHYTTWPPGVPSPASFLNLFKVRSGSLSPH 208
QY 179 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIQTADQLR 238
DB 209 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIQTADQLR 268
QY 239 FSYLAVIEGAKFTMGD 254
DB 269 FSYLAVIEGAKFTMGD 284

RESULT 4
US-08-036-210-5
Sequence 5, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SHO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-036-210-5

Query Match

99.2% Score 1336; DB 1: Length 385;

Best Local Similarity 99.2% Pred. No. 1.1e-134;
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DEPRVAKLPKNNRNPNRYSPFTHSRKIKLHEDNDYINASLTKMEFAORSYITLGGPL 60
DB 23 DEPRVAKLPKNNRNPNRYSPFTHSRKIKLHEDNDYINASLTKMEFAORSYITLGGPL 88
QY 61 PNTGHEWEMWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 120
DB 89 PNTGHEWEMWEDKSGVYMLNRYMEKSLKCAQYWPQKEKEMIFEDTNLKLTLISED 148
QY 121 IKSYTV--TELENLTTOETREILHEHYTTWPPGVPSPASFLNLFKVRSGSLSPH 178
DB 149 IKSYTVQLLENLITJQETREILHEHYTTWPPGVPSPASFLNLFKVRSGSLSPH 208
QY 179 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIQTADQLR 238
DB 209 GPVVVHCAGIGRGTCTADTCLLMKRRKDPSSVDIKKVLLEMRKFMGLIQTADQLR 268
QY 239 FSYLAVIEGAKFTMGD 254
DB 269 FSYLAVIEGAKFTMGD 284

RESULT 5
US-08-449-609-5
Sequence 5, Application US/08449609
Patent No. 5552212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SHO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-449-609-5

Query Match

99.2% Score 1336; DB 2: Length 385;

Best local similarity 99.2% Prod. No. 1,141,341
 Matches 243 Conserved 0 Mismatches 0 Indels 2 Gaps 1

QY 1 DEPCVAKLPRKNNNNRYVNSPFOHSRPTKHQEDNINYNASTIKMEFAKSYLLTQGPL 60
 DB 29 DPICGVAKLPRKNNNNRYVNSPFOHSRPTKHQEDNINYNASTIKMEFAKSYLLTQGPL 88
 QY 61 PNTGCHFWMEWVWOKSRGVMLNPKVMEKGSIKCAQVWYQKPEKKMPEYMIKLTISED 120
 DB 89 PNTGCHFWMEWVWOKSRGVMLNPKVMEKGSIKCAQVWYQKPEKKMPEYMIKLTISED 148
 QY 121 IKSYTV--TELENTTQETRELLHFHYTWDPGVPSFASPLNLFVRESGSLSPER 178
 DB 149 IKSYTVKQLELENTTQETRELLHFHYTWDPGVPSFASPLNLFVRESGSLSPER 208
 QY 179 GVVVHSSAGICTGCRSGTFCIALDLMKRRKDPSSVDIKKVLLEMRKFRMGLQTAD 238
 DB 209 GVVVHSSAGICTGCRSGTFCIALDLMKRRKDPSSVDIKKVLLEMRKFRMGLQTAD 268
 QY 236 QLRPSYLAIVEGAKFIMGD 254
 DB 269 QLRPSYLAIVEGAKFIMGD 287

RESULT 6

US-08-964-408-B
 ? Sequence 8, Application US/08964408
 ? Patent No. 6066715
 ? GENERAL INFORMATION:
 ? APPLICANT: DESMARAIS, SYLVIE
 ? APPLICANT: FRIESEN, RICHARD
 ? APPLICANT: ZAMBRONI, ROBERT
 ? APPLICANT: RAMACHANDRAN, CHIDAMBARAN
 ? APPLICANT: SKOREY, KATHRYN
 ? APPLICANT: FORD-HUTCHINSON, ANTHONY
 ? TITLE OF INVENTION: NEW LIAGANS FOR PHOSPHATASE
 ? NUMBER OF SEQUENCES: 15
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
 ? STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 ? CITY: RAHWAY
 ? STATE: NJ
 ? COUNTRY: USA
 ? ZIP: 07065
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: floppy diskette
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC DOS/MS-DOS
 ? SOFTWARE: FASTSEQ for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/964,408
 ? FILING DATE: 04 NOV 1996
 ? CLASSIFICATION: 5.10
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: NORTH, ROBERT J.
 ? REGISTRATION NUMBER: 27,466
 ? REFERENCE/DOCKET NUMBER: 19840 PCT
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 732-594-7262
 ? TELEFAX: 732-594-4720
 ? INDEX:
 ? INFORMATION FOR SEQ ID NO: 8:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 422 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MULTIPLE TYPE: peptide
 ? US-08-964-408-B

Query Match 99.2% Score 114.59 DB 1 Length 322
 Best local similarity 99.2% Prod. No. 1,141,341
 Matches 243 Conserved 0 Mismatches 1 Indels 2 Gaps 2

QY 1 DEPCVAKLPRKNNNNRYVNSPFOHSRPTKHQEDNINYNASTIKMEFAKSYLLTQGPL 60
 DB 29 DPICGVAKLPRKNNNNRYVNSPFOHSRPTKHQEDNINYNASTIKMEFAKSYLLTQGPL 88
 QY 61 PNTGCHFWMEWVWOKSRGVMLNPKVMEKGSIKCAQVWYQKPEKKMPEYMIKLTISED 120
 DB 89 PNTGCHFWMEWVWOKSRGVMLNPKVMEKGSIKCAQVWYQKPEKKMPEYMIKLTISED 148
 QY 121 IKSYTV--TELENTTQETRELLHFHYTWDPGVPSFASPLNLFVRESGSLSPER 178
 DB 149 IKSYTVKQLELENTTQETRELLHFHYTWDPGVPSFASPLNLFVRESGSLSPER 208
 QY 179 GVVVHSSAGICTGCRSGTFCIALDLMKRRKDPSSVDIKKVLLEMRKFRMGLQTAD 238
 DB 209 GVVVHSSAGICTGCRSGTFCIALDLMKRRKDPSSVDIKKVLLEMRKFRMGLQTAD 268
 QY 236 QLRPSYLAIVEGAKFIMGD 254
 DB 269 QLRPSYLAIVEGAKFIMGD 287

RESULT 7

US-08-964-313-B
 ? Sequence 8, Application US/08964413
 ? Patent No. 6114132
 ? GENERAL INFORMATION:
 ? APPLICANT: DESMARAIS, SYLVIE
 ? APPLICANT: FRIESEN, RICHARD
 ? APPLICANT: GRESSER, MICHAEL
 ? APPLICANT: KENNEDY, BRIAN
 ? APPLICANT: NICHOLSON, DONALD
 ? APPLICANT: RAMACHANDRAN, CHIDAMBARAN
 ? APPLICANT: SKOREY, KATHRYN
 ? APPLICANT: FORD-HUTCHINSON, ANTHONY
 ? TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
 ? NUMBER OF SEQUENCES: 15
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
 ? STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 ? CITY: RAHWAY
 ? STATE: NJ
 ? COUNTRY: USA
 ? ZIP: 07065
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: diskette
 ? COMPUTER: IBM compatible
 ? OPERATING SYSTEM: DOS
 ? SOFTWARE: FASTSEQ for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/964,313
 ? FILING DATE: 04 NOV 1997
 ? CLASSIFICATION: 4.35
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 60/040,408
 ? FILING DATE: 04 NOV 1996
 ? APPLICATION NUMBER: PCT/CA97/00825
 ? FILING DATE: 03 NOV 1996
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: DURETTE, PHILIPPE L.
 ? REGISTRATION NUMBER: 35,125
 ? REFERENCE/DOCKET NUMBER: 19824Y
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 732-594-4568
 ? TELEFAX: 732-594-4720
 ? INDEX:
 ? INFORMATION FOR SEQ ID NO: 8:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 322 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MULTIPLE TYPE: peptide
 ? US-08-964-313-B

Query Match 97.6%; Score 1314.5; DB 3; Length 322;
 Host Local Similarity 97.7%; Prod. No. 176-132;
 Matches 253; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

QY 1 DEPCVAKIPKKNRNRRDVSPEPDSRIKLIHQENDYINASLIKMEFAORSYILTGPL 60
 DB 29 DEPCVAKIPKKNRNRRDVSPEPDSRIKLIHQENDYINASLIKMEFAORSYILTGPL 88
 QY 61 PNTGCHFEWMEWEEKSRGVVMIINVMKESLKAQYWPQKEKEKEMIFEDTNLKLTLISED 120
 DB 89 PNTGCHFEWMEWEEKSRGVVMIINVMKESLKAQYWPQKEKEKEMIFEDTNLKLTLISED 148
 QY 121 IKSYYTV--LELENITTORELLIHFHYTTPDPCVPESPASFLNPLFKVRESGLSPRH 178
 DB 149 IKSYYTVHOLELNTIYETRELLIHFHYTTPDPCVPESPASFLNPLFKVRESGLSPRH 208
 QY 179 GIVVHCSAGI--GKSTFELATPILLMFKRPPSSVDIKVLLFMRPFMGITOTAD 235
 DB 209 GIVVHCSAGIQTGCRSTPCIAETGIIIMOKKRPSSVDIKVLLFMRPFMGITOTAD 268
 QY 236 QLEPSYLAIVIEGAKFTMGD 254
 DB 269 QLEPSYLAIVIEGAKFTMGD 287

RESULT 8

US-09-069-138-R
 Sequence 8, Application US/09069138

Patent No. 6348572
 GENERAL INFORMATION:
 APPLICANT: DESMARAIS, SYLVIE
 APPLICANT: DUFRESNE, CLAUDE
 APPLICANT: FRIESEN, RICHARD
 APPLICANT: LERLAND, YVES
 APPLICANT: ROY, PATRICK
 APPLICANT: YOUNG, ROBERT N.
 APPLICANT: ZAMRONI, ROBERT
 TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
 TITLE OF INVENTION: BINDING ASSAY
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
 STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 STATE: RAHWAY
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Diskette
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/069,138
 FILING DATE: 29-APR-1998
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: DURETTE, PHILIPPE L.
 REGISTRATION NUMBER: 35,125
 REFERENCE/DOCKET NUMBER: 19840YIA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 732-594-4568
 TELEFAX: 732-594-4720
 TELEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 322 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-09-069-138-R

Query Match 97.6%; Score 1314.5; DB 4; Length 322;
 Host Local Similarity 97.7%; Prod. No. 176-132;
 Matches 253; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

QY 1 DEPCVAKIPKKNRNRRDVSPEPDSRIKLIHQENDYINASLIKMEFAORSYILTGPL 60
 DB 29 DEPCVAKIPKKNRNRRDVSPEPDSRIKLIHQENDYINASLIKMEFAORSYILTGPL 88
 QY 61 PNTGCHFEWMEWEEKSRGVVMIINVMKESLKAQYWPQKEKEKEMIFEDTNLKLTLISED 120
 DB 89 PNTGCHFEWMEWEEKSRGVVMIINVMKESLKAQYWPQKEKEKEMIFEDTNLKLTLISED 148
 QY 121 IKSYYTV--LELENITTORELLIHFHYTTPDPCVPESPASFLNPLFKVRESGLSPRH 178
 DB 149 IKSYYTVHOLELNTIYETRELLIHFHYTTPDPCVPESPASFLNPLFKVRESGLSPRH 208
 QY 179 GIVVHCSAGI--GKSTFELATPILLMFKRPPSSVDIKVLLFMRPFMGITOTAD 235
 DB 209 GIVVHCSAGIQTGCRSTPCIAETGIIIMOKKRPSSVDIKVLLFMRPFMGITOTAD 268
 QY 236 QLEPSYLAIVIEGAKFTMGD 254
 DB 269 QLEPSYLAIVIEGAKFTMGD 287

RESULT 9

US-08-685-992-1
 Sequence 1, Application US/08685992

Patent No. 5912138
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMPTON, BROOK, SMITH & RYLANDS, P.C.
 STREET: TWO Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,992
 FILING DATE: 25-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,237
 REFERENCE/DOCKET NUMBER: CSHL96-03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 196 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-685-992-1

Query Match 78.7%; Score 1060; DB 2; Length 196;
 Best Local Similarity 100.0%; Prod. No. 1.3e-105;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPCRVAKLKKNNKNNRYRVSPPDHSRIKIQEDNDYINASTIKMEFAQSYLLTQGPL 60
 DB 1 DPCRVAKLKKNNKNNRYRVSPPDHSRIKIQEDNDYINASTIKMEFAQSYLLTQGPL 60

QY 61 PNTGHHWEMWEGSKSGVYMLNVMKSGSLKQAWYFQKEEKEMIFEDTNLKLITSED 120
 DB 61 PNTGHHWEMWEGSKSGVYMLNVMKSGSLKQAWYFQKEEKEMIFEDTNLKLITSED 120

QY 121 IKSYIVLELENTLTQETRELLHRYHTWDPGVESYASTLNTLKRKNGSGISPEHP 180
 DB 121 IKSYIVLELENTLTQETRELLHRYHTWDPGVESYASTLNTLKRKNGSGISPEHP 180

QY 181 VVHVSAGIGRSGTEG 196
 DB 181 VVHVSAGIGRSGTEG 196

RESULT 10
 US-09-144-925-1
 Sequence 1; Application US/09144925
 Patent No. 5951979
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Millia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02421-1799
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/144,925
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/645,992
 FILING DATE: July 25, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Graham, Patricia
 REGISTRATION NUMBER: 42,227
 REFERENCE/DOCKET NUMBER: CSHU-96-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 196 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-144-925-1

Query Match 78.7%; Score 1060; DB 2; Length 196;
 Best Local Similarity 100.0%; Prod. No. 1.3e-105;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPCRVAKLKKNNKNNRYRVSPPDHSRIKIQEDNDYINASTIKMEFAQSYLLTQGPL 60
 DB 1 DPCRVAKLKKNNKNNRYRVSPPDHSRIKIQEDNDYINASTIKMEFAQSYLLTQGPL 60

QY 61 PNTGHHWEMWEGSKSGVYMLNVMKSGSLKQAWYFQKEEKEMIFEDTNLKLITSED 120
 DB 61 PNTGHHWEMWEGSKSGVYMLNVMKSGSLKQAWYFQKEEKEMIFEDTNLKLITSED 120

QY 121 IKSYIVLELENTLTQETRELLHRYHTWDPGVESYASTLNTLKRKNGSGISPEHP 180
 DB 121 IKSYIVLELENTLTQETRELLHRYHTWDPGVESYASTLNTLKRKNGSGISPEHP 180

QY 181 VVHVSAGIGRSGTEG 196
 DB 181 VVHVSAGIGRSGTEG 196

RESULT 11
 US-08-685-992-2
 Sequence 2; Application US/08685992
 Patent No. 5912138
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Millia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,992
 FILING DATE: 25-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Graham, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHU-96-03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 194 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-685-992-2

Query Match 60.2%; Score 811; DB 2; Length 194;
 Best Local Similarity 73.8%; Prod. No. 5.5e-79;
 Matches 144; Conservative 29; Mismatches 29; Indels 2; Gaps 2;

QY 1 DPCRVAKLKKNNKNNRYRVSPPDHSRIKIQEDNDYINASTIKMEFAQSYLLTQGPL 60
 DB 1 DPCRVAKLKKNNKNNRYRVSPPDHSRIKIQEDNDYINASTIKMEFAQSYLLTQGPL 59

Db 119 WKSYTVVLDLEININSGEIRRTLSHFHYTTWTFDEVCPSPASFLNFLKVFSSSLNPDHGP 178
QY 181 VVYLICSGAGISGSGTF 195
Db 179 AVIHCAGSIGCRSGTF 193

RESULT 13
US-08-446-345-27
Sequence 27, Application MS/08446345

RESULT 13
 US-08-446-345-27
 Sequence 27, Application us/08446345
 Patent No. 5831099
 GENERAL INFORMATION:
 APPLICANT: Ulitch, Axel
 APPLICANT: Moller, Niels P.H.
 APPLICANT: Moller, Karin B.
 TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
 TITLE OF INVENTION: PHOSPHATASES PTP-D1
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: N.Y.
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,345
 FILING DATE: 22-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/234,440
 FILING DATE: 28-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30742
 REFERENCE/DOCKET NUMBER: 7683-054
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 866-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-446-345-27

Query Match	45.7%	Score 616:	DB 2:	Length 120:
Best Local Similarity	98.3%	Pred. No. 2e-58:	0:	Mismatches 2:
Matches 118:	Conservative	0:	Indels	Gaps 1:
QY	70	MWMEQKSPCVMLNRYMEKSLKCAQVMPQKREKIMLPEDTNLKLTLISDIPKSYTV--	127	
Db	1	MWMEQKSPGVMLNRYMEKSLKCAQVMPQKREKIMLPEDTNLKLTLISDIPKSYTVQ	60	
QY	128	LELENLTTQETREILFHHTTTPDQGVGESSPASFNLFLFKRSGSLSPHGPVVMHCSA	187	
Db	61	LELENLTTQETREILFHHTTTPDQGVGESSPASFNLFLFKRSGSLSPHGPVVMHCSA	120	

RESULT 14
 US-08-201-6e97-16
 Sequence ID: Application US-08c1697
 Patent No. 5705623

```

GENERAL INFORMATION:
1
2 APPLICANT: Thomas, Frederick E.
3 TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
4
5 NUMBER OF SEQUENCE: 17
6
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Campbell and Flores
9 STREET: 470 La Jolla Village Drive, Suite 700
10 CITY: San Diego
11 STATE: California
12 COUNTRY: USA
13
14 FILING DATE: 9/21/92
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC DOS/MS DOS
20 SOFTWARE: Patent in Release #1.0, Version #1.25
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/201,697
24 FILING DATE: 25 Feb 1994
25 CLASSIFICATION: 540
26
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Campbell, Anthony A.
29 REGISTRATION NUMBER: 41,845
30 REFERENCE/DOCKET NUMBER: P 08 9783
31
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (619) 545 9001
34 TELEFAX: (619) 545 8949
35
36 INFORMATION FOR SEQ ID NO: 16:
37
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 278 amino acids
40 TYPE: amino acid
41 TOPOLOGY: linear
42
43 US 08 201 697 16
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

```

```

COUNTRY: USA
1
2 ZIP: 02173
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Diskette
6
7 COMPUTER: IBM compatible
8 OPERATING SYSTEM: Windows 95
9
10 SOFTWARE: FASTSO for Windows Version 2.0b
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/685,992
14 FILING DATE: 25-JUL-1996
15
16 CLASSIFICATION: 435
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER:
20
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Graubard, Patricia
23 REGISTRATION NUMBER: 32,227
24 REFERENCE/DOCKET NUMBER: CSH196-03
25
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 781-861-6340
28 TELEFAX: 781-861-9540
29
30
31 INFORMATION FOR SEQ ID NO: 14:
32
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 254 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38
39 MOLECULE TYPE: peptide
40
41 US-08-685-992-14
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

```

Search completed: June 18, 2002, 14:56:12
Job time: 23 sec

E1 /label beta 4
 E1 /note "region of beta sheet secondary structure"
 E1 Region
 E1 89..92
 E1 /label beta 5
 E1 /note "region of beta sheet secondary structure"
 E1 Region
 E1 104..107
 E1 /label beta 6
 E1 /note "region of beta sheet secondary structure"
 E1 Region
 E1 112..120
 E1 /label beta 7
 E1 /note "region of beta sheet secondary structure"
 E1 Region
 E1 129..131
 E1 /label beta 8
 E1 /note "region of beta sheet secondary structure"
 E1 Region
 E1 138..145
 E1 /label beta 9
 E1 /note "region of beta sheet secondary structure"
 E1 Binding site
 E1 151..152
 E1 /note "residues interacting with substrates"
 E1 Region
 E1 158..170
 E1 /label alpha 3
 E1 /note "region of alpha helical secondary structure"
 E1 Region
 E1 180..183
 E1 /label beta 10
 E1 /note "region of beta sheet secondary structure"
 E1 Binding site
 E1 185
 E1 /note "residue interacting with substrate"
 E1 Binding site
 E1 187
 E1 /note "residue interacting with substrate"
 E1 Region
 E1 189..208
 E1 /label alpha 4
 E1 /note "region of alpha helical secondary structure"
 E1 Binding site
 E1 190..191
 E1 /note "residues interacting with substrates"
 E1 Region
 E1 216..224
 E1 /label alpha 5
 E1 /note "region of alpha helical secondary structure"
 E1 Binding site
 E1 232
 E1 /note "residue interacting with substrate"
 E1 Region
 E1 235..253
 E1 /label alpha 6
 E1 /note "region of alpha helical secondary structure"
 E1 W020051041 A2
 E1 21 Aug 2001
 E1 13 FEB 2001: 2001W010805180
 E1 14 FEB 2000: 2000S0181769
 E1 (CETP) CEPTYR INC.
 E1 E1001 A1, 10001 DEJ
 E1 W01: 2001 5/05/0/64
 E1 Screening assays to identify agents that alter protein tyrosine
 E1 phosphatase (PTP) binding to, and PTP mediated catalytic
 E1 dephosphorylation of phosphotyrosine peptide substrates
 E1
 E1 Disclosure: Fig 1: 7pp; English
 E1
 E1 The invention relates to identifying agents which alter the interaction
 E1 between a protein tyrosine phosphatase (PTP) and a tyrosine
 E1 phosphorylated polypeptide using fluorescence energy signals. The methods
 E1 are useful for performing screening assay to identify agents that alter
 E1 PTP binding to and ptp mediated catalytic dephosphorylation of
 E1 phosphotyrosine peptide substrates. The present sequence is that of human
 E1 PTPB
 E1
 E1 Sequence 254 AA:

Query Match 109.08; Score 1347; DH 22; Length 254;
 Best Local Similarity 100.08; Pred. No. 6,5e-126;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEICVANIIPKKNKNNKRVDSFIPDSKIKHCPNDVFNASTIKMEACSYILLQSPIL 60
 DB 1 dfervakipknknrvydsfshsrkikqendynmsikmcaqsylltqpl 60
 QY 61 PPTCGHFMWMEWEEKSRVVMENPVEKSLKCAQYWPQKEKEKIEFDTKLTISED 120
 DB 61 pteqhtwewewegksrgvymnrvemkgsikcaqwpqkeckemtdtkitlised 120
 QY 121 IKSYYVLLALNIEITIOENRELIHFHYTTPDPGVNESPASFINLPKVNIGSISPERGP 180
 DB 121 lksyyvleleelldqelrelhhytllphtqpeegastlillktrcqs-sperhp 180
 QY 181 VVHCSAGIGNSGIFCLADICLLMKRRKIDSSVDIKKVLKMKRPMGILQFAVQLPFS 240
 DB 181 vvhsagigsgfcladfccllmdtrkpfssvdlkvvlkmmktrmgllqfadqfts 240
 QY 241 YLAVIEGAKETMGD 254
 DB 241 ylaviegakrtimgd 254

RESULT 2

AAB59364
 ID AAB59364 standard; Protein: 254 AA.

AC AAB59364;

DT 21-MAR-2001 (first entry)

DE Human protein tyrosine phosphatase #1.

KW Protein tyrosine phosphatase, human, mouse, fruit fly; ptp;

KW substrate trapping.

OS Homo sapiens.

PN W0200075339-A1.

PD 14-DEC-2000.

PF 24-MAY-2000; 2000W02514211.

PR 03-JUN-1999; 990S-0137319.

PA (COLD-) (COLD SPRING HARBOR LAB.

PI Tonks NK, Zhang S;

WP1: 2001-080598/09.

PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in

PT which the wild type PTP catalytic domain invariant aspartate is

PT replaced with an unphosphorylated amino acid, useful in gene therapy

PS Disclosure: Fig 1: 10pp; English.

CC The present invention provides substrate trapping mutant protein tyrosine

CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine

CC phosphorylated proteins and to screen for modulators capable of altering

CC the binding of protein tyrosine phosphatases to their substrate. These

CC may be used in disease diagnosis and treatment.

SQ Sequence 254 AA:

Query Match 99.58; Score 1340; DH 22; Length 254;

Best Local Similarity 99.68; Pred. No. 3.4e-125;

Matches 254: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 DEPCRVAKIIPKNNKNNRYRVSPEPDSRIKIHQEDNDYINASLIMKEAQRSYLTGQPL 60
 DB 1 dpcrvaklprknnknrrydrvsdpdsrirkhqedndyinaslkmeeaqrsylltqpl 60
 OY 61 PNTGHEWEMWEDKSRGVVNLNRYMEKGSILKAYWPFQKEEKMEIEDNLKLTISED 120
 DB 61 pntghehwemwedsrgrvvnlnrymekgsilkaaywfpqkeekmiednlkltsied 120
 OY 121 IKSYYTV--LELENTTQETREILHFHYTTPDQGVPESPASFLNPLFKVRESGSLSPHH 180
 DB 121 iksyytv--lelenttqetrelhfhyyttpdqgvpepsasflnplfkvresgslsphh 180
 OY 181 VVHVHCSAGICRSGTFCPLADICLIMKKKQSSVPIKKVILMMKRPKMLIGTANQIPRS 240
 DB 181 vvvhvcsagiqrsgrtfcpladclimkkqssvpikkvilmmkrpkmliigtanqiprs 240
 OY 241 YLAVIEGAKPTMGD 254
 DB 241 ylaviegaktimgd 254

RESULT 3
 AAR13907
 ID AAR13907 standard: Protein: 435 AA.

XX AC AAR13907:
 XX DT 28-NOV-1991 (first entry)
 XX DE Human protein phosphotyrosyl phosphatase PTPBH.
 XX KW PTPase B1; growth suppression activity; ANL; myeloproliferation.
 XX OS Homo sapiens.
 XX FN W09113173-A.
 XX PD 05-SEP-1991.
 XX PF 01-MAR-1991: 91WO-0001432.
 XX PR 18-JAN-1991: 91US-0643041.
 XX PR 02-MAR-1990: 90US-0487733.
 XX PA (B107-) APPL BIOTECHN INC.
 XX PI Brusklin AM, Hill DE;
 XX DR WPI: 1991-281485/38.
 XX DR N-USDB: AAN13643.
 XX PT Vector contg. protein phospho-tyrosyl phosphatase gene (fragment
 XX PT for use in diagnosis of cancers; e.g. acute non-lymphocytic
 XX PT leukaemia)
 XX PS Claim 6: Fig 1; 73pp; English.
 XX CC A human placental cDNA library was screened with degenerate probes
 XX CC deduced from the partial amino acid sequence of the PTPase 1B (see
 XX CC AA013653 and AA013654 for probe sequences); one recombinant
 XX CC bacteriophage hybridised to both probes and was shown to contain a
 XX CC 3.2 kb fragment. The fragment was subcloned in pCM33 and sequenced
 XX CC The open reading frame was predicted to encode this 435 amino acid
 XX CC protein. The calculated mol. wt. is 49,966. PTPBH is useful for
 XX CC treatment of ANL; myelodysplastic syndrome and myeloproliferative
 XX CC disorders. See also AA013644-013654.
 XX SO Sequence 435 AA;

Query Match 99.2%; Score 1336; DB 12; Length 435;

Best Local Similarity 99.2%; Pred. No. 1,76 124;
 Matches 254, Conservative 0: Mismatches 0: Indels 2: Gaps 1:

OY 1 DEPCRVAKIIPKNNKNNRYRVSPEPDSRIKIHQEDNDYINASLIMKEAQRSYLTGQPL 60
 DB 29 dpcrvaklprknnknrrydrvsdpdsrirkhqedndyinaslkmeeaqrsylltqpl 88
 OY 61 PNTGHEWEMWEDKSRGVVNLNRYMEKGSILKAYWPFQKEEKMEIEDNLKLTISED 120
 DB 89 pntghehwemwedsrgrvvnlnrymekgsilkaaywfpqkeekmiednlkltsied 148
 OY 121 IKSYYTV--LELENTTQETREILHFHYTTPDQGVPESPASFLNPLFKVRESGSLSPHH 178
 DB 149 iksyytv--lelenttqetrelhfhyyttpdqgvpepsasflnplfkvresgslsphh 208
 OY 179 GVHVHCSAGICRSGTFCPLADICLIMKKKQSSVPIKKVILMMKRPKMLIGTANQIPRS 238
 DB 209 gvhvvhcsagiqrsgrtfcpladclimkkqssvpikkvilmmkrpkmliigtanqiprs 268
 OY 239 FSYLAVIEGAKPTMGD 254
 DB 269 fsy laviegaktimgd 284

RESULT 4
 AAM51206
 ID AAM51206 standard: Protein: 435 AA.

XX AC AAM51206:
 XX DT 19-DEC-2001 (first entry)
 XX DE Human PTPBH Genbank Accession Number P18031
 XX KW PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
 XX KW dephosphorylation; phosphotyrosine; human: PTPBH.
 XX OS Homo sapiens.
 XX FN W0200161031-A2.
 XX PD 23-AUG-2001.
 XX PF 13-FEB-2001: 2001WO-0505180.
 XX PR 14-FEB-2000: 2000US-0181769.
 XX PA (CEPT-) CEPTYR INC.
 XX PI Flint AJ, Cool DE;
 XX DR WPI: 2001-570570/64.
 XX PT Screening assays to identify agents that alter protein tyrosine
 XX PT phosphatase (PTP) binding to, and PTP-mediated catalytic
 XX PT dephosphorylation of phosphotyrosine peptide substrates
 XX PS Example 1: Page 7; 79pp; English.

XX CC The invention relates to identifying agents which alter the interaction
 XX CC between a protein tyrosine phosphatase (PTP) and a tyrosine
 XX CC phosphorylated polypeptide using fluorescence energy signals. The methods
 XX CC are useful for performing screening assay to identify agents that alter
 XX CC PTP binding to and PTP-mediated catalytic dephosphorylation of
 XX CC phosphotyrosine peptide substrates. The present sequence is not given in
 XX CC the specification but is that of human PTPBH protein sequence taken from
 XX CC Genbank (Accession Number: P18031). The present sequence was used to
 XX CC generate mutants E181A (AAM51203) and C215S (AAM51204) as described in
 XX CC the specification.
 XX CC Note: An alternative sequence for human PTPBH is given in figure 1 of
 XX CC the specification (AAG/8262).

Sequence 435 AA;

Query Match	Score	Length
100% Identity Similarity	99.246	1416
Matches: 2544	Conservative: 0	Mismatches: 0
		Indels: 2
		Gaps: 0

XX	RESISTANCE
XX	AAP01948
1D	AAP00648 standard; Protein; 45% AA.
XX	
XX	AAP00648:
1E	
1F	25 SEP 2001 (first entry)
XX	
1E	Human protein phosphatase-1B (PTP1B).
XX	
KW	Human protein phosphatase-1B (PTP1B); antisense; gene therapy;
KM	infection; inflammation; tumor; prophylaxis.
XX	
OS	Hemo-Sapiens.
XX	
FN	US6,261,840 B1.
XX	
17	1 JUL 2001.
1E	
1E JAN 2000; 2000MS 048766H.	
XX	
1E JAN 2000; 2000MS 048766H.	
XX	
PA	(US13) US13 PHARM INC.
1E	
1E	Cowsett LM, Weart JJ.
1E	MPLS 2001 432181/46.
XX	N EST00; AAP01946.
XX	
1E	New antisense compounds capable of modulating expression of human
1E	protein phosphatase-1B; useful for diagnosis, prophylaxis and treatment
1E	of diseases associated with expression of protein phosphatase -
XX	
XX	Example 14; Column 55-60; 7HP; English.
XX	
1E	The invention is directed to antisense compounds, particularly
1E	oligonucleotides which are targeted to a DNA encoding protein
1E	phosphatase 1B (PTP1B) to modulate its expression. The antisense
1E	compounds are useful for diagnosis, prophylaxis and treatment of
1E	diseases associated with the expression of PTP1B, to prevent or
1E	delay infection, inflammation and tumor formation and as a
1E	research reagent. The PTP1B DNA is useful in gene therapy.
XX	The present sequence is human PTP1B protein.
1E	Sequence 435' AA:

	Query Match	Similarity	99.2%	Score 1346	Id 22	Length 4353
	Best Local	Similarity	99.2%	Prod. No. 1,70	124	
	Matches	254	Conservative	0	Mismatches	0
					Indels	2
					Gaps	1
QY	1	DFFPVPAAKLPNNKNPNRYDVSPEFHSTRIKLHQEDNDYIMNSLTKMEEDAKSYILLTQVPL	60			
DB	29	dlfrvvaaklpnkknrnyrdsfphstriklnghndyfnsltkmcaagisylltqpl	88			
QY	61	PNTHKPKFWKPKSKSVVMNKNMKNSTKCAVWQCNKPKMKEEDTNKLKLSKD	120			
DB	89	plnthkpkfwkpkssvvmnknmknstkgvwhkpkemkeldtnklkllsed	148			
QY	121	IKSYIVV--LEENLITTOFTRELIHFHTTWIDGVPSTASTNFIKKVRQNSLSPEH	178			
DB	149	lksyivtqltlenlttqetcdlftlytqfdgvspsstnrtkkvrsnsspeh	208			
QY	179	GPVVVHFSVAGTFRSTETPLATQETILMKPKPKSVETIKYVLLFMKPTMMLQTAQGLR	238			
DB	209	gpvvvhsaagtsagttcladctclmckkdpssvcdkksclcmkltmglsqadqtl	268			
QY	239	FSYLAIVHGAQKPIMGD	254			
DB	269	tsylaivhgaqkilmgd	284			

CC	XX	RESULT	6
CC	XX	AAM51203	
CC	XX	ID	AAM51203 standard; Protein; 435 AA.
CC	XX	AC	
CC	XX	AA	AAM51203:
CC	XX	D1	19-DEC-2001 (first entry)
CC	XX	DE	Human PTP1B mutant D181A.
CC	XX	PTP	Protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
CC	XX	KM	dephosphorylation; phosphotyrosine; human; PTP1B; metcine; mutant.
CC	XX	Homo sapiens.	
CC	XX	Synthetic.	
CC	XX	Key	Location/Qualifiers
CC	XX	Misc-difference 181	
CC	XX	/note	"Wild-type Asp substituted by Ala"
CC	XX	W0200161031-A2.	
CC	XX	23-AUG-2001.	
CC	XX	13-FEB-2001; 2001MO-US05180.	
CC	XX	14-FEB-2000; 2000MS_0181769.	
CC	XX	(CEPT-) CEPTYR INC.	
CC	XX	P1int AD; Cool DE;	
CC	XX	WEI; 2001-570570/64.	
CC	XX	Screening assays to identify agents that alter protein tyrosine	
CC	XX	phosphatase (PTP) binding to, and PTP-mediated catalytic	
CC	XX	dephosphorylation of phosphotyrosine peptide substrates	
CC	XX	Example 1, Page 79pp; English.	

The invention relates to identifying agents which alter the interaction between a protein tyrosine phosphatase (PTP) and a tyrosine phosphorylated polypeptide using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter PTP binding to and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is that of a

Wavelength, μ	Refractive index, n_D	Optical density, D_{545}
400	1.5000	0.0000
410	1.4998	0.0000
420	1.4995	0.0000
430	1.4992	0.0000
440	1.4989	0.0000
450	1.4986	0.0000
460	1.4983	0.0000
470	1.4980	0.0000
480	1.4977	0.0000
490	1.4974	0.0000
500	1.4971	0.0000
510	1.4968	0.0000
520	1.4965	0.0000
530	1.4962	0.0000
540	1.4959	0.0000
550	1.4956	0.0000
560	1.4953	0.0000
570	1.4950	0.0000
580	1.4947	0.0000
590	1.4944	0.0000
600	1.4941	0.0000
610	1.4938	0.0000
620	1.4935	0.0000
630	1.4932	0.0000
640	1.4929	0.0000
650	1.4926	0.0000
660	1.4923	0.0000
670	1.4920	0.0000
680	1.4917	0.0000
690	1.4914	0.0000
700	1.4911	0.0000
710	1.4908	0.0000
720	1.4905	0.0000
730	1.4902	0.0000
740	1.4899	0.0000
750	1.4896	0.0000
760	1.4893	0.0000
770	1.4890	0.0000
780	1.4887	0.0000
790	1.4884	0.0000
800	1.4881	0.0000
810	1.4878	0.0000
820	1.4875	0.0000
830	1.4872	0.0000
840	1.4869	0.0000
850	1.4866	0.0000
860	1.4863	0.0000
870	1.4860	0.0000
880	1.4857	0.0000
890	1.4854	0.0000
900	1.4851	0.0000
910	1.4848	0.0000
920	1.4845	0.0000
930	1.4842	0.0000
940	1.4839	0.0000
950	1.4836	0.0000
960	1.4833	0.0000
970	1.4830	0.0000
980	1.4827	0.0000
990	1.4824	0.0000
1000	1.4821	0.0000

Query Match	54.9%	Score 726.5	108.22	Length 535
Best Local Similarity	56.6%	Prod. No. 14663		
Matches	147	Conserved 42	Mismatches 56	Indels 7
				Gaps 2

07	12	NRNNRNRVNSRPNRNRKIKRQHNINQVNSAKIKMFAQSRVYILIQDQIPNRQCHEWEMV	7
10b	60	metatrypanpdyshsivlrkrtsvdylnanbhqylacrgylltqgplvdvqghfelmv	119
07	72	WEGKSRVVMQNRQMPKRNKIKALYWIYKREKEMIFETNKKLTISEDKRSYTVL---	128
10b	120	WSPKSLAVLIMIKRMKRPKIVRthlypncmzadkakikpvrkivcyvrltelyqpfvtyw	179
07	129	ELNNLPLQGRRELHPEVYILWQRPQVNSPASKINLPEKVRSGSLSPHGVYVHGSA	187
10b	180	IKKIKLDELQSPHRCVGMTHYILWPDQIPSPHNAIKIKIYVRDSQCISRDQAPVVMGSA	239
07	188	GLIKNSGILPPTABDQVILMDRQVQSVSWLPEKVLIPMRFPWGLIQTANQLPESYLAIVEG	247
10b	240	qutpsstfctvdcvclvdkyqcvmsvkvltvolsymmqitqsdqitstysatlcq	296
27	248	AK 249	
10b	297	IK 298	

Submitted (revised) 10/1/02; Accepted 1/26, 2002; 14:56:48
 Date of time: 5/9/2002

A:Cross-references: GB:140595; NID:q75042; P1DN:AAA64615.1; P1D:q75043
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:40-266/Domains: protein-tyrosine-phosphatase homology <apps>
 F:215/Active site: Cys (phosphotyrosine intermediate) *status predicted
 F:221/Binding site: substrate phosphate (Arg) *status predicted

Query Match 95.8%; Score 1290; DB 1; Length 432;
 Host Local Similarity 94.5%; Pred. No. 1c-97; Indels 2; Gaps 1;
 Matches 242; Conservative 9; Mismatches 3

DB 1 DEPCVAVAKLPKKNRRYDVSPFDHSRIKIQEDNDYINASTIMEEDQORSYITQGPL 60
 |||||
 DB 29 DPCVAVAKLPKKNRRYDVSPFDHSRIKIQEDNDYINASTIMEEDQORSYITQGPL 88
 |||||
 DB 41 DPTGCHHEWMEWQSRGVVMLNRYMEKSLKCAQYVWQKEKEMIFEDTNIKLITLSED 120
 |||||
 DB 89 PNTGCHHEWMEWQSRGVVMLNRYMEKSLKCAQYVWQKEKEMIFEDTNIKLITLSED 148
 |||||
 DB 121 IKSYTYV--LEFNITQTRRLIHPHTTMDPGVPESPASHNPLFKVRSGSLSPRH 178
 |||||
 DB 149 VMSYIVKQLEHLENTKRELIHPHTTMDPGVPESPASHNPLFKVRSGSLSPRH 208
 |||||
 DB 179 GPVAVHSAITGSGTCTATGTLILMKRKPSSVYIKVLEMPKFMGLTQTADQLR 236
 |||||
 DB 209 GPVAVHSAITGSGTCTATGTLILMKRKPSSVYIKVLEMPKFMGLTQTADQLR 268
 |||||
 DB 239 FSYLAVIEGAKFTMGD 254
 |||||
 DB 259 FSYLAVIEGAKFTMGD 284
 |||||

RESULT - 4
 JMW0049
 protein-tyrosine-phosphatase (EC 3.1.3.48) 1 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 03-Dec-1999
 C:Accession: JMW0049

R:Jung, K.J.; Kang, Y.S.; Kim, C.W.
 Biochem. Biophys. Res. Commun. 246, 239-242, 1998
 A:Title: Multiple phosphorylation of chicken protein tyrosine phosphatase 1 and human p1
 A:Reference number: JMW0049; MIMD:98262948
 A:Accession: JMW0049
 A:Molecule type: mRNA
 A:Residues: 1-356 <JMW>
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase
 C:Keywords: phosphoric monoester hydrolase
 F:27-253/Domains: protein-tyrosine-phosphatase homology <FT>

Query Match 94.4%; Score 1271; DB 2; Length 356;
 Host Local Similarity 93.4%; Pred. No. 2.8c-96; Indels 2; Gaps 1;
 Matches 239; Conservative 10; Mismatches 5

DB 1 DEPCVAVAKLPKKNRRYDVSPFDHSRIKIQEDNDYINASTIMEEDQORSYITQGPL 60
 |||||
 DB 16 DPCVAVAKLPKKNRRYDVSPFDHSRIKIQEDNDYINASTIMEEDQORSYITQGPL 75
 |||||
 DB 61 PNTGCHHEWMEWQSRGVVMLNRYMEKSLKCAQYVWQKEKEMIFEDTNIKLITLSED 120
 |||||
 DB 76 PNTGCHHEWMEWQSRGVVMLNRYMEKSLKCAQYVWQKEKEMIFEDTNIKLITLSED 135
 |||||
 DB 121 IKSYTYV--LEFNITQTRRLIHPHTTMDPGVPESPASHNPLFKVRSGSLSPRH 178
 |||||
 DB 146 IKSYTYVLENDLENTKRELIHPHTTMDPGVPESPASHNPLFKVRSGSLSPRH 195
 |||||
 DB 176 GPVAVHSAITGSGTCTATGTLILMKRKPSSVYIKVLEMPKFMGLTQTADQLR 238
 |||||
 DB 196 GPVAVHSAITGSGTCTATGTLILMKRKPSSVYIKVLEMPKFMGLTQTADQLR 255
 |||||
 DB 239 FSYLAVIEGAKFTMGD 254
 |||||

DB 256 FSYLAVIEGAKFTMGD 271

RESULT 5
 S14294
 protein-tyrosine-phosphatase (EC 3.1.3.48) 11A rat

C:Species: Rattus norvegicus (Norway Rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S14294; S21831
 R:Swarn, G.; Kamakur, S.; Kadha, V.; Kema, V.
 FEBS Lett. 280, 65-69, 1991
 A:Title: Molecular cloning and expression of a protein-tyrosine phosphatase showing h
 A:Reference number: S14294, MIMD:31184422
 A:Accession: S14294
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-363 <SWA>
 A:Cross-references: GB:X58828; NID:q56045; P1DN:AAA1643.1; P1D:q56996
 R:Swarn, G.; Kamakur, S.; Kadha, V.; Kema, V.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S21831
 A:Accession: S21831
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-363 <SWA>
 A:Cross-references: EMBL:X58828; NID:q56045; P1DN:AAA1643.1; P1D:q56996
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase
 C:Keywords: alternative splicing; DNA binding; phosphoprotein; phosphoric monoester h
 F:42-264/Domains: protein tyrosine phosphatase homology <apps>
 F:216/Active site: Cys (phosphotyrosine intermediate) *status predicted
 F:222/Binding site: substrate phosphate (Arg) *status predicted

Query Match 75.3%; Score 1014; DB 1; Length 363;
 Host Local Similarity 71.9%; Pred. No. 2.8c-75; Indels 6; Gaps 3;
 Matches 184; Conservative 38; Mismatches 28

DB 1 DEPCVAVAKLPKKNRRYDVSPFDHSRIKIQEDNDYINASTIMEEDQORSYITQGPL 60
 |||||
 DB 31 DPCVAVAKLPKKNRRYDVSPFDHSRIKIQEDNDYINASTIMEEDQORSYITQGPL 90
 |||||
 DB 61 PNTGCHHEWMEWQSRGVVMLNRYMEKSLKCAQYVWQKEKEMIFEDTNIKLITLSED 120
 |||||
 DB 91 PNTGCHHEWMEWQSRGVVMLNRYMEKSLKCAQYVWQKEKEMIFEDTNIKLITLSED 149
 |||||
 DB 121 IKSYTYV--LEFNITQTRRLIHPHTTMDPGVPESPASHNPLFKVRSGSLSPRH 178
 |||||
 DB 150 VKSYTYVHLLQLENINSGETRTISHHTTMDPGVPESPASHNPLFKVRSGSLSPRH 209
 |||||
 DB 179 GPVAVHSAITGSGTCTATGTLILMKRKPSSVYIKVLEMPKFMGLTQTADQLR 238
 |||||
 DB 210 GPVAVHSAITGSGTCTATGTLILMKRKPSSVYIKVLEMPKFMGLTQTADQLR 266
 |||||
 DB 239 FSYLAVIEGAKFTMGD 254
 |||||
 DB 257 FSYLAVIEGAKFTMGD 282
 |||||

RESULT 6

A33899
 protein-tyrosine-phosphatase (EC 3.1.3.48) 1 - human
 N:Alternative names: protein-tyrosine-phosphatase, T-cell specific
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1990 #sequence_revision 02-May-1994 #text_change 07-May-1999
 C:Accession: A33899; C60145; A45142
 R:Cooper, D.E.; Tock, N.K.; Charbonneau, B.; Walsh, K.A.; Fischer, E.H.; Krebs, E.G.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5257-5261, 1989
 A:Title: cDNA isolated from a human T cell library encodes a member of the protein-ty
 A:Reference number: A33899; MIMD:89315776
 A:Accession: A33899
 A:Molecule type: mRNA
 A:Residues: 1-415 <COO>
 A:Cross-references: GB:M25393

[illegible]

A:Reference label: A46101; MUID:93216607
A:Accession: B46101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1 548 <MCID>
A:Cross-references: GB:L11251
A:Note: authors translated the codon TTT for residue 482 as Ile
C:Genelocs:
A:Gene: Flybase:PF061P
A:Cross-references: Flybase:FBgn0003138
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type PTP6P, protein tyrosin
C:Keywords: alternative splicing; phosphoprotein, phosphoric monoester hydrolase, tyro
F:607-285/Domain: protein-tyrosine-phosphatase homology <PTP>
F:637/Active site: cys (phosphotyrosine intermediate) #status predicted
F:243/Binding site: substrate phosphate (Arg) #status predicted

```

Query: March 1994, Score 725.51, DB 2: Length 548;
Best Local Similarity 556.68, Pred. No. 1,7e-51;
Matches 137: Conservative 42; Mismatches 56; Indels 7; Gaps 2;

QY 12 NRRNRPPVPSVPHDSPIKTHQPNINYNASTIKMTAQSSTYITIOCHLINTGCHWMMV 71
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 NRGALNPVPQNPVGHSPITVLRKGSVWYINANIYDLERAEERYIITIOGFLVTVHEWLMV 119
QY 72 MRUKSGVYMLNRWVEKSKICQAWPOKEEMFEETNTKLTLEISPIKSYTVL--- 128
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 WROKSAVALINAKMLWKKQIKCHLWPMENKADKAKLPYKATITVELVRIITQYNNPRW 179
QY 129 -ELENTTQETPEILPHFYTTWPDQGVPESPAFNLTLEKVRSSGSIPEHGPPVYHCSA 187
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 180 FKLTLEIYQSSREVMFHTTITPDEGIESPMALKEFQGVVDSGSLSRGTAIVHCSA 239
QY 188 GYSSRSPTPLATGCTLIMKPKIPSSVIAKKVILKMRKRMQILQTAQILPFSYLAIVG 247
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 240 GHSRSSTPLVETVITVLIDKY---SGCNVSKVLDELRTYRMQLIQTADQDPSVALIEG 296
QY 248 AK 249
   |
DB 297 IK 298

RESULT 11
A:Accession: A53978
Protein: Tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX1 - African clawed f
C:Species: Xenopus laevis (African clawed frog)
C:Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 24-Apr-1998
C:Accession: A53978
P:DOI Vercchio, R.L.; Tonks, N.K.
I:J Biol. Chem. 269, 19639-19645, 1994
A:Title: Characterization of two structurally related Xenopus laevis protein tyrosine
A:Reference number: A53978; M01D:94308257
A:Accession: A53978
A:Status: Preliminary
A:Molecule type: mRNA
A:Features: 1-694 <DEL>
A:Experimental source: ovary
A:Note: Sequence extracted from NCI backbone (NCIIN:149756, NCIIN:149758)
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3, cellular retinaldehyde;
C:Keywords: phosphoprotein, phosphoric monoester hydrolase, tyrosine-specific phosphat
F:38-227/Domain: cellular retinaldehyde-binding protein homology <CR>
F:425-661/Domain: protein-tyrosine phosphatase homology <PT>
F:614/Active site: Cys (phosphocysteine intermediate) #status predicted
F:619/Binding site: substrate phosphate (Arg) #status predicted

```


A:Accession: S17671
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-583 <GEN>
 A:Cross-references: EMBL:X58289
 R:Heinrichs, W.; Brugman, G.; Janssen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein tyrosine phosphatases
 A:Reference number: S40280
 A:Accession: S40287
 A:Molecule type: mRNA
 A:Residues: 377-497, 747-485-486 <GEN>
 A:Cross-references: EMBL:X52355; NID:9438149; PIRN:CA80591.1; PID:9458150
 C:Superfamily: protein-tyrosine phosphatase, receptor type 44a; fibronectin type III re-
 C:Key words: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot-
 E:111-536/Domain: protein tyrosine phosphatase homology (PTP)
 E:1488/Active site: Cys (phosphocysteine intermediate) #status predicted
 E:1494/Binding site: substrate phosphate (Arg) #status predicted

Query Match 36.9%; Score 496.5; DB 2; Length 583;
 Best Local Similarity 41.5%; Pred. No. 9, 2e-33;

Matches 102; Conservative 47; Mismatches 82; Indels 15; Gaps 6;

QY 4 GNAAKLPKNNKNNRYSPDHSRIKLNQD---NDYINASTLKMWAQSPYITVGP 59
 DB 303 GDAIIFENKRNKNRYNITPYDSEVKLSNVDDPTSDYINASTPNNRPYITVGP 362
 QY 60 LPNTGHEWENWVQKSPVVMNFMVWERSLKCQAYWQKEKEKEMFEDTNKLTILSE 119
 DB 363 LPCKIDPFWMAHQNHNIMVIVQCEKGRKCDHWMPADDDPIYQD--LIDQMVSE 419
 QY 120 DKSSTVLELENTTQET---REILHNTTPDDEGVSPSPSLNLFLEKRESSLSLP 176
 DB 420 SYLEWITPEFKTCEPQLNHPHTFTVWPDHGVPTTQSLTQFTVTDYINRSP 479
 QY 177 FHGIVVWVSGAGVGRSGFCLADTCLLMDKKRPSSVDLKKVLLMKRPMGLTQTAQ 236
 DB 480 GAGSVVHGAGVGRITFVALDRILOGLDSK--DSVDIYGAVHDFLRHVNVTQ--E 534
 QY 237 LRESYL 242
 DB 535 QGVVYL 540

RESULT 15

D41214 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 10a, short splice form precursor

C:Species: Drosophila melanogaster
 C:Date: 28 May 1992 #sequence_revision 28 May 1992 #text_change 23-Jun-1999

C:Accession: D41214; #sequence_revision 28 May 1992 #text_change 23-Jun-1999
 R:Yang, X.; Seow, K.T.; Bahrl, S.M.; Oon, S.H.; Chia, W.
 Cell 67, 661-673, 1991

A:Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sub-

A:Reference number: A41214; MUID:92034988

A:Accession: D41214
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA
 A:Residues: 1-1557 <YAN>

A:Cross-references: GR:M80465
 R:Lin, S.S.; Janssen, P.; Zinn, K.
 Cell 67, 675-685, 1991

A:Title: Three receptor-linked protein-tyrosine phosphatases are selectively expressed c

A:Reference number: A41215; MUID:92034989

A:Accession: A41215
 A:Molecule type: mRNA
 A:Residues: 1-904, 117, 906, 1125, 1126, 1126, 1165, 1166, 1171, 1171, 1173-1215, 1173, 1217-1456,

A:Cross-references: GR:M80538; NID:9158644; PIRN:AAA28952.1; PID:9158645
 C:Genes: FLYBASE:FBgn004370

A:Gene: FLYBASE:FBgn004370
 A:Cross-references: FLYBASE:FBgn004370
 C:Superfamily: protein-tyrosine-phosphatase, receptor type 4b; fibronectin type III re-
 C:Key words: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recep-

F:1197-1213/Domain: transmembrane #status predicted <GEN>
 F:1214-1557/Domain: intracellular #status predicted <GEN>
 F:1295-1515/Domain: protein-tyrosine phosphatase homology #status predicted
 F:1467/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1473/Binding site: substrate phosphate (Arg) #status predicted

Query Match 46.8%; Score 492.5; DB 2; Length 1557;
 Best Local Similarity 39.1%; Pred. No. 6, 7e-32;

Matches 104; Conservative 45; Mismatches 90; Indels 27; Gaps 6;

QY 1 DPCGVAKLPKNNKNNRYSPDHSRIKLNQD---NDYINASTLKMWAQSPYITVGP 56
 DB 1244 LQYCTFAIDPCNHRKNNRYNITPYDSEVKLSNVDDPTSDYINASTPNNRPYITVGP 1343
 QY 57 GSPLENTGHEWENWVQKSPVVMNFMVWERSLKCQAYWQKEKEKEMFEDTNKLTILSE 110
 DB 1344 GSPLENTGHEWENWVQKSPVVMNFMVWERSLKCQAYWQKEKEKEMFEDTNKLTILSE 1394
 QY 111 NKTITLSDIKSYTVLELENTTQET---REILHNTTPDDEGVSPSPSLNLFLEKRESSLSLP 170
 DB 1395 DIKVITLSDIKSYTVLELENTTQET---REILHNTTPDDEGVSPSPSLNLFLEKRESSLSLP 1454
 QY 171 SGSLSPHGVVWVSGAGVGRSGFCLADTCLLMDKKRPSSVDLKKVLLMKRPMGLTQTAQ 230
 DB 1455 --RICAQRPVHVHCSAGVGRSGFCLADTCLLMDKKRPSSVDLKKVLLMKRPMGLTQTAQ 1509
 QY 431 LQYCTFAIDPCNHRKNNRYNITPYDSEVKLSNVDDPTSDYINASTPNNRPYITVGP 56
 DB 1510 VQYCTFAIDPCNHRKNNRYNITPYDSEVKLSNVDDPTSDYINASTPNNRPYITVGP 1535

Search completed: June 18, 2002, 14:57:14

Job time: 85 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:55:50 ; Search time 11.04 Seconds
(without alignments)
890 R30 Million cell updates/sec

Title: US-09-788-626-2

Perfect score: 1347
Sequence: 1 DFGCRVAKIIPKKNKNNPWW - DQIIGSYIAVIRKAKFIMQD 254

Scoring table: BLOSUM62
Gapop 10.0, capex 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SWISSProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	99.2	435	1 PPTN_HUMAN	P18031 homo sapien
2	1315	97.6	432	1 PPTN_RAT	P20417 rattus norv
3	1299	96.4	432	1 PPTN_MOUSE	P35821 mus musculu
4	1278	94.9	434	1 PPTN_CHICK	O13016 gallus gall
5	1014	75.3	463	1 PPTN_RAT	P35233 rattus norv
6	1011	75.1	415	1 PPTN_HUMAN	G06180 mus musculu
7	1008	74.8	382	1 PPTN_MOUSE	P17706 homo sapien
8	498.5	37.0	1997	1 PPTN_HUMAN	P23467 homo sapien
9	492.5	36.6	1630	1 PPTN_MOUSE	P35992 drosophila
10	480	35.6	377	1 PPTN_HUMAN	P34138 dictyostell
11	474	35.2	1337	1 PPTN_MOUSE	P35235 mus musculu
12	469.5	34.9	585	1 PPTN_MOUSE	P35842 drosophila
13	469	34.8	1301	1 PPTN_MOUSE	O06124 homo sapien
14	468.5	34.8	593	1 PPTN_HUMAN	P43378 homo sapien
15	467	34.7	593	1 PPTN_HUMAN	P41499 homo sapien
16	465.5	34.6	593	1 PPTN_MOUSE	P23470 mus musculu
17	464.5	34.5	1445	1 PPTN_MOUSE	O64455 mus musculu
18	462	34.3	1238	1 PPTN_MOUSE	O05909 mus musculu
19	461.5	34.3	1442	1 PPTN_MOUSE	O98948 gallus gall
20	458.5	34.0	1122	1 PPTN_MOUSE	P10586 homo sapien
21	457.5	34.0	595	1 PPTN_MOUSE	P26045 homo sapien
22	455.5	33.8	1897	1 PPTN_HUMAN	P29350 homo sapien
23	452	33.6	913	1 PPTN_HUMAN	P29074 homo sapien
24	447.5	33.2	595	1 PPTN_HUMAN	P28827 mus musculu
25	441.5	32.8	926	1 PPTN_MOUSE	P28828 mus musculu
26	441	32.7	1452	1 PPTN_MOUSE	P24468 homo sapien
27	441	32.7	1452	1 PPTN_MOUSE	P18433 homo sapien
28	440.5	32.7	1912	1 PPTN_HUMAN	O12923 homo sapien
29	437.5	32.5	802	1 PPTN_HUMAN	O03348 rattus norv
30	435.5	32.3	2485	1 PPTN_HUMAN	P23352 mus musculu
31	434.5	32.3	796	1 PPTN_MOUSE	P23469 homo sapien
32	430	31.6	802	1 PPTN_MOUSE	
33	429	31.8	700	1 PPTN_HUMAN	

Result ID	Score	Query Match	Length	DB ID	Description
34	427	31.7	699	1 PPTN_MOUSE	P49446 mus musculu
35	423	31.4	1439	1 PPTN_HUMAN	O15262 homo sapien
36	420	31.2	780	1 PPTN_HUMAN	O05209 homo sapien
37	420	31.2	979	1 PPTN_MOUSE	O06673 mus musculu
38	420	31.2	1304	1 CD45_HUMAN	P08575 homo sapien
39	418.5	31.1	2314	1 PPTN_HUMAN	P23471 homo sapien
40	418	31.0	1152	1 CD45_MOUSE	P06800 mus musculu
41	416.5	30.9	2029	1 LAR_DROME	P16621 drosophila
42	416	30.9	775	1 PPTN_MOUSE	P35831 mus musculu
43	416	30.9	1001	1 PPTN_MOUSE	P08560 mus musculu
44	416	30.9	1004	1 PPTN_MOUSE	O63475 rattus norv
45	416	30.9	1457	1 PPTN_MOUSE	P35822 mus musculu

ALIGNMENTS

Result ID	Score	Query Match	Length	DB ID	Description
AC	418031	US0904	US0904	1 PPTN_HUMAN	STANDARD: PPT: 435 AA.
DT	01-NOV-1990	(Rel. 16, Created)			
DT	01-NOV-1990	(Rel. 16, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, last annotation update)			
DE	protein-tyrosine phosphatase, non receptor type 1 (PC 3.1.3.48)				
DE	(protein-tyrosine phosphatase 1b) (PTP-1b).				
DE	PTP1B OR PTP1B.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI:taxid:9606;				
RN	[1]				
RP	SEQUENCE FROM N A				
RC	TISSUE=Placenta;				
EX	MEDLINE=30207/7; PubMed=215711.				
KA	Chernoff J., Schievella A.R., Jost C.A., Erikson R.L., Neel H.C.;				
RT	Cloning of a cDNA for a major human protein-tyrosine phosphatase.;				
RI	Proc. Natl. Acad. Sci. U.S.A. 87:2735-2739(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
EX	MEDLINE=301140; PubMed=216424;				
KA	Brown-Shiner S., Johnson K.A., Lawrence J.B., Johnson C.;				
KA	Brusklin A., Green N.R., Hill D.E.;				
RT	Molecular cloning and chromosome mapping of the human gene encoding				
RT	protein-tyrosine phosphatase 1b.;				
PL	Proc. Natl. Acad. Sci. U.S.A. 87:5148-5152(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
KA	Deonkas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.;				
KA	Jones M., Stavrides G., Almeida J.P., Barbade A.K., Baqanley C.L.;				
KA	Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.;				
KA	Beasley O.F., Bird C.P., Blakey S.F., Bridgman A.N., Brown A.J.;				
KA	Huck D., Burdill W., Butler A.P., Carter C., Carter N.P.;				
KA	Chapman J.C., Clapp M., Clark C., Clark L.N., Clark S.Y., Clee G.M.;				
KA	Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.P.;				
KA	Coulson A., Corliffe G.J., Deafman R., Dhami P., Dunn M.;				
KA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.;				
KA	Graham D.V., Griffiths C., Griffiths M.N.D., Galliam R., Hall R.E.;				
KA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.;				
KA	Huckle E., Hunt A.K., Hunt S.R., Jakobsen K., Johnson C.M., Johnson D.;				
KA	Kay M.P., Kimberley A.M., King A., Knighs A., Latif G.K., Lawlor S.;				
KA	Marshall M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.;				
KA	Marsh V.L., Martin S.L., McDonachie L.J., Mclay K., Murray A.A.;				
KA	Malne S., Mistry D., Moore M.T., Mullikin J.C., Nickerson T.;				
KA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.;				
KA	Phillimore H.J.C.T., Prachinang S.R., Plumb R.W., Ramsay H.;				
KA	Rice C.M., Ross M.P., Scott C.E., Schra R.K., Showkden R., Sims S.;				
KA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Stinson J.E.;				
KA	Swann M., Symantre N., Taylor F., Tee L., Thomas D.W., Thorpe A.;				
KA	Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.;				
KA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.;				
KA	Wimling L., Wray P.W., Hubbard T., Durbin R.M., Bentley R.R., Brock S.;				

111 PROTEIN DNA SEQUENCE AND COMPARATIVE ANALYSIS OF HUMAN CYTOSOLIC 20.
 112
 113 Nature 414:660-661(1991).
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616

```

CC          entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC          or send an email to license@sib-sib.ch).
CC
CC          EMBL: M31724; AAA60223.1; -
DR          EMBL: M33689; AAA60157.1; -
DR          EMBL: M33684; AAA60158.1; -
DR          EMBL: M33688; AAA60158.1; JOINED.
DR          EMBL: M33687; AAA60158.1; JOINED.
DR          EMBL: M33686; AAA60158.1; JOINED.
DR          EMBL: M33685; AAA60158.1; JOINED.
DR          EMBL: AL034429; CAC34283.1; -
DR          EMBL: AL013230; CAC00618.1; -
DR          EMBL: NC015660; AAH15660.1; -
DR          PIR: A35992; TP00N1.
DR          PDB: 2HNQ; 20-DEC-94.
DR          PDB: 1PTT; 01-AUG-96.
DR          PDB: 1PTU; 01-AUG-96.
DR          PDB: 1PTV; 01-AUG-96.
DR          PDB: 1PTV; 21-JAN-98.
DR          PDB: 1AAX; 04-MAR-98.
DR          PDB: 1A5Y; 17-JUN-98.
DR          PDB: 1BZC; 16-FEB-99.
DR          PDB: 1BZH; 16-FEB-99.
DR          PDB: 1BZJ; 16-FEB-99.
DR          MIM: 176885; -
DR          InterPro: IPR000340; DS_phosphatase.
DR          InterPro: IPR000387; TYR_phosphatase.
DR          InterPro: IPR000242; TYR_prot_kinphatase.
DR          Pfam: PF00102; V_phosphatase.
DR          PRINTS: PR00700; PR00PHPTASE.
DR          SMART: SM00194; ptpcc; 1.
DR          SMART: SM00012; ptpcc_DSG; 1.
DR          PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR          PROSITE: PS00384; TYR_PHOSPHATASE_2; 1.
DR          PROSITE: PS00056; TYR_PHOSPHATASE.
DR          PROSITE: PS00055; TYR_PHOSPHATASE_ptp; 1.
DR          Hydroclass: Acetylation; Phosphorylation; 3D-structure.
KT          MOD_RES 1 288 ACETYLATION.
FT          DOMAIN 40 288 PROTEIN-TYROSINE PHOSPHATASE.
FT          ACT_SITE 215 215 PHOSPHORYLATION.
FT          MOD_RES 352 352 PHOSPHORYLATION (HY PRG).
FT          MOD_RES 378 378 PHOSPHORYLATION (HY CMC2).
FT          MOD_RES 386 386 PHOSPHORYLATION (HY CMC2).
SO          SOURCE 435 AA; 4966 MW; 802377DCD33F41FD CRY64;

Query Match 99.28; Score 1336; DB 1; Length 445;
Best local similarity 99.28; Pred. No. 1,60-112;
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1

QY 1 EFPRVAALEPKKRNRRFGVSPETDLSKILHFNQVYNANLKNMFVQPSYLLIQGL 60
DB 29 DEPRFVAALPKKRNRRFGVSPFHSFLKIQEDNDYINASLIMKEEAPSYILLQGL 88
QY 61 PNICGHEHFWMEQKSPSVMI NPWFQSGIKCAQWYQGEPEKPMIFPPNNLKLIISD 120
DB 89 PRTGCHFEHFWMEQKSPSVVMI NPWFQSGIKCAQWYQGEPEKEMIFEDTNLKLIISD 148
QY 121 IKSYYTV--LELENTLTQETREILHIVITWDPGVSPSPASLNLFEKVRSGSLSPH 178
DB 149 IKSYYTVQMLENTLTQETREILHIVITWDPGVSPSPASLNLFEKVRSGSLSPH 208
QY 179 GPVVVHGNGSTGSPSTFVLATGCLLMKPKPPSSVPIKKVLLPMPFPFMGLIQNTAQLE 238
DB 209 GPVVVHGNSAGTSPSTFVLADPTLLMKPKPPSSVDIKKVL EMLKPEPMGLIQNTAQLE 268
QY 239 FSYLAVIIGAKFTMGD 254
DB 269 FSYLAVIIGAKFTMGD 284

RESULT 2
PRTN_RAT

```

ID PNTL.MOUSE STANDARD: PRT: 432 AA.
 AC P20417;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 1b) (PTP-1b).
 GN PTPN1.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID:10116;
 DX NCBI_TaxID:10116;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-90160454; PubMed-2154749;
 RA Guan K., Han R.S., Watson S.J., Geahlen R.L., Dixon J.F.;
 RT "Cloning and expression of a protein-tyrosine-phosphatase."
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1501-1505(1990).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA
 CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS
 CC THE CYTOPLASM.
 CC -1- TISSUE SPECIFICITY: FOUND IN SEVERAL TISSUES INCLUDING CENTRAL
 CC NERVOUS SYSTEM, LIVER AND KIDNEY. A HIGH LEVEL OF EXPRESSION WAS
 CC FOUND IN THE HIPPOCAMPI.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMRL: M3962; AAC79516.1; -
 DR PIR: A14845; A14845.
 DR HSSP: P18041; 1PTV.
 DR InterPro: IPR000340; DS-phosphatase.
 DR InterPro: IPR000347; TYR-phosphatase.
 DR InterPro: IPR000242; TYR-prot-phphatase.
 DR Pfam: PF00102; X-phosphatase.1.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPC.1.
 DR SMART: SM00012; PTPC_DSPC.1.
 DR SMART: PS00383; TYR_PHOSPHATASE_1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2.1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP.1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2.1.
 KM Hydrophobic. 43 238
 FT DOMAIN 215 215 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 215 215 BY SIMILARITY.
 FT SPOUNCE 432 AA 40074 MW: 106565000Da 188cst CR64:
 Query Match 97.64; Score 13.5; DB 1; Length 432;
 Best Local Similarity 95.78; Pred. No. 1,2e-110;
 Matches 245; Conservative 7; Mismatches 2; Indels 2; Gaps 1;
 QY 1 DPGHVAALPKNNKNNRYDVSIPDHSLKIHQHNQYNASLLKMEFAQSYLLTGGPL 60
 DB 29 DEPCIALPLPNKNPNPFCVSPDHSPFKLHQENQYNASLLKMEFAQSYLLTGGPL 88
 QY 61 PNTCHHEHMEWQSKSGVVLNKKVNGSLNCAQYWFQKEKLMIFETN;KITL;SEED 120
 DB 89 PNTCHHEHMEWQSKSGVVLNKKVNGSLNCAQYWFQKEKLMIFETN;KITL;SEED 148
 QY 121 IKSYTVV-LELENTLTQETREILHFTTTWDFGVPSPASFLNFKVWESGSLSEH 178
 DB 149 VASVYTVQIILENLATQFARELIHPHYTTWDFGVPSPASFLNFKVWESGSLSEH 208

QY 179 GPVYVHCASGICSGHPCADTCLLMKRRKDSYDIKKVLEMKRFMGLTQTADQLR 238
 DB 209 GPVYVHCASGICSGHPCADTCLLMKRRKDSYDIKKVLEMKRFMGLTQTADQLR 268
 QY 239 FSVIATVEGAKFTMGD 254
 DB 269 FSVIATVEGAKFTMGD 284
 RESULT 3
 PNTL.MOUSE STANDARD: PRT: 432 AA.
 ID PNTL.MOUSE
 AC P35821; G62131; G63840; G64498; G99JST1;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 1b) (PTP-1b) (Protein-tyrosine
 DE phosphatase HA2) (PTP-HA2).
 GN PTPN1.
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID:10090;
 DX NCBI_TaxID:10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE-92328784; PubMed-1378268;
 RA Miyasaka H., Li S.S.L.;
 RT "The cDNA cloning, nucleotide sequence and expression of an
 RT intracellular protein tyrosine phosphatase from mouse testis."
 RT Biochem. Biophys. Res. Commun. 185:818-825(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liao K., Lane M.D.;
 RT Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA Park K., Byun S.;
 RT Submitted (MAY 1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 102-213 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE-9513432; PubMed-7832766;
 RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
 RT "A novel receptor-type protein tyrosine phosphatase with a single
 RT catalytic domain is specifically expressed in mouse brain."
 RT Biochem. J. 305:499-504(1995).
 RN [5]
 RP SEQUENCE OF 161-432 FROM N.A.
 RA Strausberg R.;
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA
 CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS
 CC THE CYTOPLASM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN TESTIS. ALSO FOUND IN KIDNEY,
 CC SPLEEN, MUSCLE, LIVER, HEART AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMRL: M97590; -; NOT ANNOTATED_CDS.
 DB EMBL: L40595; AAA64615.1; -


```

01-1-1994 (Rel. 28, Created)
01-1-1994 (Rel. 28, Last sequence update)
01-1-1994 (Rel. 34, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP-S).
CN ptpn2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10115;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=脾脏;
RX MEDLINE=91184422; PubMed=1849097;
RA Swarp G.; Kamatkar S.; Radha V.; Renu V.;
RT "Molecular cloning and expression of a protein-tyrosine phosphatase
RT showing homology with transcription factors Fos and Jun."
RL FEBS Lett. 280:65-69(1991).
RN [2]
RP DNA-BINDING;
RX MEDLINE=93183863; PubMed=8443161;
RA Radha V.; Kamatkar S.; Swarp G.;
RT "Binding of a protein-tyrosine phosphatase to DNA through its
RT carboxy-terminal noncatalytic domain."
RL Biochemistry 32:2194-2201(1993).
RN [3]
RP FUNCTION: BINDS SINGLE-STRANDED AND DOUBLE-STRANDED DNA WITH HIGH
CC NONSPECIFIC AFFINITY THROUGH ITS C-TERMINAL REGION.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: DOES NOT SHOW VARIABILITY. MACROPHAGES
CC SHOWED HIGHER LEVELS OF EXPRESSION THAN LYMPHOCYTES.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcements/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X58828; CAA41633.1;
DR PIR: S14294; S14294.
DR PIR: S21831; S21831.
DR HSSP: P18031; 2HNO.
DR InterPro: IPR000387; Tyr_Phosphatase.
DR InterPro: IPR000242; Tyr_Prot_Phphtase.
DR Pfam: PF00102; Y_phosphatase_1.
DR PRINTS: PR00700; PRTYPHPHTASE.
DR SMART: SM00194; PTPC.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
DR KEGG: K04422; TYR_PTP.
DR KEGG: K04422; TYR_PTP.
DR ACT_SITE 216 216 BY SIMILARITY.
DR DNA_BIND 326 359 BASIC MOTIF (POTENTIAL).
DR SHOUNCE 353 AA; 42236 MW; B417C0446024715 CDS;

```

Query Match 75.38; Score 1014; DB 1; Length 363;
 Best Local Similarity 71.98; Freq. No. 183;
 Matches 184; Conservative 38; Mismatches 28; Indels 6; Gaps 4;

```

01-1-1994 (Rel. 28, Created)
01-1-1994 (Rel. 28, Last sequence update)
01-1-1994 (Rel. 34, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP-S).
CN ptpn2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10115;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=脾脏;
RX MEDLINE=91184422; PubMed=1849097;
RA Swarp G.; Kamatkar S.; Radha V.; Renu V.;
RT "Molecular cloning and expression of a protein-tyrosine phosphatase
RT showing homology with transcription factors Fos and Jun."
RL FEBS Lett. 280:65-69(1991).
RN [2]
RP DNA-BINDING;
RX MEDLINE=93183863; PubMed=8443161;
RA Radha V.; Kamatkar S.; Swarp G.;
RT "Binding of a protein-tyrosine phosphatase to DNA through its
RT carboxy-terminal noncatalytic domain."
RL Biochemistry 32:2194-2201(1993).
RN [3]
RP FUNCTION: BINDS SINGLE-STRANDED AND DOUBLE-STRANDED DNA WITH HIGH
CC NONSPECIFIC AFFINITY THROUGH ITS C-TERMINAL REGION.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: DOES NOT SHOW VARIABILITY. MACROPHAGES
CC SHOWED HIGHER LEVELS OF EXPRESSION THAN LYMPHOCYTES.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcements/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X58828; CAA41633.1;
DR PIR: S14294; S14294.
DR PIR: S21831; S21831.
DR HSSP: P18031; 2HNO.
DR InterPro: IPR000387; Tyr_Phosphatase.
DR InterPro: IPR000242; Tyr_Prot_Phphtase.
DR Pfam: PF00102; Y_phosphatase_1.
DR PRINTS: PR00700; PRTYPHPHTASE.
DR SMART: SM00194; PTPC.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
DR KEGG: K04422; TYR_PTP.
DR KEGG: K04422; TYR_PTP.
DR ACT_SITE 216 216 BY SIMILARITY.
DR DNA_BIND 326 359 BASIC MOTIF (POTENTIAL).
DR SHOUNCE 353 AA; 42236 MW; B417C0446024715 CDS;

```

```

DB 91 PNTQCHFWLWVWQKTRAVVYVNLKTVKPSVKAQYWP- (ID:RMRVKEIGFYSKLI)SD 149
QY 121 IKSYYIV--LELENLTQETREILHFTTTWPGVGESEASNTLFPKRESLSPEH 178
DB 150 VKSYVTHLLQLENNINSGETRTISHFTYTPDGEVSESPASFLNLFKRESGLNPDH 209
QY 179 GPVAVHSCAGISGSGCPGLADTCLIMDKKRPDSSVILIKVILHRRFERMCILOTAOLR 238
DB 210 GPVAVHSCAGISGSGTSLVPTTLVLMKEKED---VAVKQTLISMRKRYMLIOTPOLR 266
QY 239 FSYLVATGAKFIMGD 254
DB 267 FSYVALLKCAKVKTKD 282

```

```

RESULT 6
PNT2_HUMAN STANDARD; PRT; 415 AA.
ID P17706; Q96HR2;
AC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48) (T-
DE cell protein-tyrosine phosphatase) (TCPP).
CN ptpn2 OR PTPP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=89315776; PubMed=2546150;
RA Cool D.; Toxns N.; Chabonneau B.; Walsh K.; Fischer E.H.; Krebs E.G.;
RT "cDNA isolated from a human T-cell library encodes a member of the
RT protein-tyrosine-phosphatase family."
RL Proc. Natl. Acad. Sci. U.S.A. 86:5257-5261(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92115688; PubMed=1731319;
RA Mosinger B. Jr.; Tillmann U.; Westphal H.; Tremblay M.L.;
RT "Cloning and characterization of a mouse cDNA encoding a cytoplasmic
RT protein-tyrosine-phosphatase."
RL Proc. Natl. Acad. Sci. U.S.A. 89:499-503(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM PTPB).
RC TISSUE=Eye;
RA Strausberg R.;
RT Submitted (MAY-2001) to the EMBL/Genbank/DDBJ databases.
CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O -> protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: PTPA AND PTPB (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PTPA ISOFORM IS PROBABLY THE MAJOR PTP
CC EXPRESSED IN HUMAN TISSUES. PTPB ISOFORM WAS FOUND IN T-CELLS AND
CC IN PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcements/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M25393; AAA65997.1;
DR EMBL: M81478; NOT ANNOTATED_CDS.
DR EMBL: BC008244; AA08244.1;
DR PIR: A33899; A33899.
DR HSSP: P18031; PTPY.

```


0X MBL TaxID-9606:
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Placenta;
 RX MEDLINE-91060118: pubmed-2170109;
 RA Krieger N X., Streiff M., Salto H.;
 FT structural diversity and evolution of human receptor-like protein
 tyrosine phosphatases.";
 RI LMO J. 9:3241-3252(1990).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein
 tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC This SWISS-prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC
 CC EMBL: X54131; CAA38066.1;
 DR PIR: S12050; S12050.
 DR HSP: P18052; 1YFO.
 DR MIM: 176882;
 DR InterPro: IPR0033961; FN111.
 DR InterPro: IPR000387; TYR-phosphatase.
 DR InterPro: IPR000242; TYR-Frol-phphatase.
 DR Pfam: PF00041; In3; 16.
 DR Pfam: PF00102; Y-phosphatase; 1.
 DR PRINTS: PR00700; PR1YPHPHAS.
 DR SMART: SM00060; FRS; 15.
 DR SMART: SM00164; PRPH1.
 DR PROSITE: PS00344; TYR-PHOSPHATASE_1;
 DR PROSITE: PS00056; TYR-PHOSPHATASE_2; 1.
 DR PROSITE: PS00055; TYR-PHOSPHATASE_FTP; 1.
 KW Glycoprotein; Transmembrane; Hydrolyase; Phosphorylation; Repeat;
 KW Signal;
 FT SIGNAL 1 22 POTENTIAL;
 FT CHAIN 23 1997 PROTEIN-TYROSINE PHOSPHATASE BETA.
 FT DOMAIN 23 1621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1622 1642 POTENTIAL.
 FT DOMAIN 1643 1997 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 23 110 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 111 200 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 201 286 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 287 374 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 375 464 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 465 551 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 552 640 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 641 728 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 729 816 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 817 904 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 905 992 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 993 1082 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 1083 1170 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 1171 1268 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1269 1352 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 1353 1442 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 1443 1997 PROTEIN-TYROSINE PHOSPHATASE
 FT ACT_SITE 1904 1904 BY SIMILARITY.
 FT CARBOHYD 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 479 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 652 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 721 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 829 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1040 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1096 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1470 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1474 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SQUIDNCE 1997 AA, 224267 MW, 631P49HA7A151519 Cys64;
 Query Match 37.0%; Score 498.5; DB 1; Length 1997;
 Host local Similarity 41.5%; Pred. No. 1,9e-36;
 Matches 102; Conservative 48; Mismatches 81; Indels 15; Gaps 6;
 QY 4 CRVAKLPKNNRRNRYVSPDISRIKLHED---NDYINASLIKMEFGRSYTLTQGP 59
 Db 1719 CDIALLEPDKRKNYNNILPYDATRKLSNVDPPGSDYINASTYPPNNRRREVLTQGP 1778
 QY 60 LPNIGCFHWGFWFQKRSQVMI NRWVKEGSI KCAQYWPQKEKEMF PEDFINIKETLISE 119
 Db 1779 LPGRKDFPKWKNVQNNVNIYMTQUCVEKRGVKCDHWF ATGSLVYGD--LLQMLSE 1835
 QY 120 DIKSYVTVLEIENLTQET---RELIPIHTTWPPRPVSPASFLNFLFVRESGSLSP 176
 Db 1836 SVLPDWMTIRPEKICGPFQLAHKRLIRHHYHVTWPDHGHETQSLDQVKTVAIVYINSP 1895
 QY 177 EHGIVVWVCSAGIGRSPTPLATFVLLMEKPKPSSVFIKKVLEMKRFMS;LQVADQ 236
 Db 1896 GAVTVVWVSGVSPPTFTIALPFTIQGLSK---DSVTFYGAVIDRLAHVHWVQT--E 1950
 QY 237 LRFPSYL 242
 Db 1951 GQVYVL 1956
 RESULT 9
 ID PRP1_DROME STANDARD: PRP1; 1630 AA.
 AC P35992;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase 10D precursor (RC 3.1.3.48) (Receptor-
 linked protein-tyrosine phosphatase 10D).
 OS PRP10D.
 GN Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Phytomyza; Neoptera; Megoptera; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidae; Diptera; Drosophilidae; Drosophila.
 CC NCHI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE-Embryo;
 RC MEDLINE-92034989; pubmed-1657402;
 RA Tian S.-S., Tsoufas P., Zinn K.;
 FT "Three receptor-linked protein-tyrosine phosphatases are selectively
 expressed on central nervous system axons in the Drosophila embryo.";
 FT Cell 67:675-685(1991).
 FT [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE-Embryo;
 RC MEDLINE-92034988; pubmed-1657401;
 RA Yang X., Seow K.T., Bahrl S.M., Don S.H., Chia M.;
 FT "Two Drosophila receptor-like tyrosine phosphatase genes are

F1	FARMO (HYD)	4.78	4.78	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	44.2	44.2	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	4.1	4.1	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	4.76	4.76	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	4.91	4.91	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	4.96	4.96	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	4.4	4.4	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	4.41	4.41	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	5.01	5.01	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	5.25	5.25	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	5.36	5.36	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	5.02	5.02	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	6.04	6.04	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	6.18	6.18	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	6.28	6.28	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	6.7	6.67	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	6.6	6.66	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	6.9	6.9	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	7.1	7.1	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	7.2	7.2	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	7.84	7.84	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	7.93	7.93	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	8.24	8.24	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	9.13	9.13	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	9.47	9.47	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	26.1	26.1	N LINKED (GLC'NAc' - -)	(POTENTIAL)
F1	FARMO (HYD)	9.8	9.7	N LINKED (GLC'NAc' - -)	(POTENTIAL)
20	STUDY IN THE	14.47 AA.	14.47 AA.	YANKELETSKY, D. - LOWENSTICHEL, (IN REF. 2)	
				MEM. BIOCHIM. 1942, 106, 67-64.	

[illegible]

RT "SH2-containing phosphotyrosine phosphatase as a target of protein
 RT tyrosine kinases."
 RL Science 259:1607-1611(1993).
 RN 121.
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS) OF 4-103.
 RX MEDLINE 94363243; PubMed-752135;
 RA Lee C.-H., Kominos D., Jacques S., Margolis B., Schlessinger J.,
 RA Shoelson S.E., Kuriyan J.;
 RI "Crystal structures of peptide complexes of the amino-terminal SH2
 RI domain of the Src tyrosine phosphatase."
 R4 Structure 2:423-438(1994).
 CC -1- FUNCTION: THIS PTPASE ACTIVITY MAY DIRECTLY LINK GROWTH FACTOR
 CC RECEPTORS AND OTHER SIGNALING PROTEINS THROUGH TYROSINE
 CC PHOSPHORYLATION. THE SH2 REGIONS MAY INTERACT WITH OTHER CELLULAR
 CC COMPONENTS TO MODULATE ITS OWN PHOSPHATASE ACTIVITY AGAINST
 CC INTERACTING SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2O) -> protein
 CC tyrosinate + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED BY TYROSINE-PROTEIN KINASES.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. SUBCLASS THAT CONTAINS SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL institution
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, usage by and for commercial
 CC entities requires a license agreement (<http://www.ebi.ac.uk/EDB/doc/miscellaneous/copyright.html>) or send an email to license@ebi.scrib.ch.
 CC
 DE EMBL: L06663; NOT_ANNOTATED_CDS.
 DE PIR: A46209; A46209.
 DR PDG: IAYA; 31-AUG-94.
 DR PDG: IAYB; 31-AUG-94.
 DR PDG: IAYC; 31-AUG-94.
 DR PDG: IAYD; 31-AUG-94.
 DR MCB: MG1:99511; Ptpn11.
 DR InterPro: IPR0009480; SH2.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000242; Tyr_ptot_phphatase.
 DR Pfam: PF00101; SH2_2.
 DR Pfam: PF00102; Y-phosphatase; 1.
 DR PRINTS: PR00700; PTPTPTPTPTASE.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR SMART: SMO0194; PTPc; 1.
 DR SMART: SMO0152; SH2_2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00386; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 1.
 DR PROSITE: PS00011; SH2_2.
 KW Hydrolyase; SH2 domain; Repeat; phosphorylation; 3d-structure.
 FT DOMAIN 6 102
 FT DOMAIN SH2 1.
 FT DOMAIN 112 216
 FT DOMAIN 276 521
 FT ACCT_SITE 463
 FT ACCT_SITE MY SIMILARITY.
 SC SOURCEFAM 585 AA; 66416 MW; 665554f929bf72a cpo64;

Query Match	34.9%	Score 469.5	Dr 1	Length 585
Best Local Similarity	37.8%	Pred. 1.5e-34		
Matches	96	Conservative	50	Mismatches 89
			Indels	2
			Gaps	4

QY	11	KNKNRVRDPSFPHSRKIKLHED	----	NIYNASLTKM	-----	FAGRSYLIQ	57
Db	272	ENKKNRPKNLIPGUTVVVLH	QPPRPVSV	INDNIIMFFPR	KNNKSKRKSTATQ		341
QY	58	GPIDPITQCFWMEWQKSPQYVM	INPVKCSL	KCAQYWDPRSKFM	IFPM	NLKTLL	117
Ldb	332	QCLQNTFMDPMMHVPQGNRPV	VMTRKRV	QWPKSKCYKPM	----	DEYALKEGVMMVENV	388
QY	118	SEDIKSYVLELE	-----	NLTQETKEIL	IFHYTTPWDG	GVESVASFNL	170

```

Db 389 KESANIDTLEKLSKVSQALLQINTERVWQYHFRWPDHGVSDSGVLDLEEVIII 448
QY 171 SCSLSPHCPVAVVHCAGIGRSCGFCIANICLIMKKNKVSVCIRKVLILMRKFRMC: 230
Db 449 KOESTVDMSPVAVVHCAGIGRSCGFCIANICLIMKKNKVSVCIRKVLILMRKFRMC: 508
QY 231 IGTADQIFRSTYLAIV 244
Db 509 VQTFADYRFTYMAV 522

RESULT 13
PTP9_DROME STANDARD: FRI, 1301 AA.
ID PTP9_DROME
AC P35832:
DT 01-JUN-1994 (rel. 29, Created)
DT 01-JUN-1994 (rel. 41, Last sequence update)
DE 01-MAR-2002 (rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase 99A precursor (EC 3.1.3.48) (Receptor-linked protein-tyrosine phosphatase 99A).
GN PTP99A.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phlebotoma; Neoptera; Endopterygota; Lepidoptera; Brachyoptera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11
RP SOURCE FROM N.A.
RC TISSUE-Eye, imaginal disk;
RX MEDLINE=92107940; PubMed=1662390;
RA Haribaran I.K., Chuang P.-L., Rubin G.M.;
RT Cloning and characterization of a receptor class phosphotyrosine phosphatase gene expressed on central nervous system axons in Drosophila melanogaster.
RT Proc Natl Acad Sci U S A 88:11266-11270(1991).
RL [3]
RN 12
RP SOURCE FROM N.A.
RC TISSUE-embryo;
RX MEDLINE=92034985; PubMed=1657402;
RA Tian S.-S., Tsoulfas P., Zinn K.;
RT Three receptor-linked protein-tyrosine phosphatases are selectively expressed on central nervous system axons in the Drosophila embryo.
RT Cell 67:661-665(1991).
RN 13
RP SOURCE FROM N.A.
RC TISSUE-embryo;
RX MEDLINE=92034985; PubMed=1657401;
RA Yang X., Seow K.T., Bahri S.M., Oon S.H., Chia W.;
RT Two Drosophila receptor like tyrosine phosphatase genes are expressed in a subset of developing axons and pioneer neurons in the embryonic CNS.
RT Cell 67:661-665(1991).
CC -1- FUNCTION: MAY PLAY A KEY ROLE IN SIGNAL TRANSDUCTION AND GROWTH
CC -1- CONTROL.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O -> protein tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS THAT DIFFER IN THEIR C-TERMINAL TAILS ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN TYROSINE PHOSPHATASE DOMAINS.
CC This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

```

```

DR EMBL: M81795; AAA28483.1; -
DR EMBL: M80359; AAA28485.1; -
DR EMBL: M80464; AAA28486.1; -
DR FTR: A41622; A41622
DR FTR: A41214; A41214
DR FTR: B41214; B41214
DR FTR: B41215; B41215
DR HSSP: P18052; 1YFO.
DR P1Phase; P890004369; PTP99A.
DR InterPro; IPR003361; FN_111.
DR InterPro; IPR003362; FN111_repeat.
DR InterPro; IPR000187; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_prol_phphatase.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y-phosphatase; 2.
DR PRINTS; PR00014; FNTYPT11.
DR PRINTS; PR00700; PRTPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM0194; PTP; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_2; 1.
KW Transmembrane; Hydrophobic; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 79
FT CHAIN 30 1301
FT DOMAIN 30 392
FT TRANSMEM 393 416
FT DOMAIN 417 1301
FT DOMAIN 64 108
FT DOMAIN 169 268
FT DOMAIN 269 368
FT DOMAIN 497 747
FT DOMAIN 748 975
FT ACT_SITE 682 682
FT DOMAIN 1076 1091
FT CARBOHYD 33 33
FT CARBOHYD 176 176
FT CARBOHYD 212 212
FT CARBOHYD 278 278
FT CARBOHYD 322 322
FT CARBOHYD 336 336
FT VAR_SEQ 1050 1119
FT CONFLICT 586 586
FT CONFLICT 1205 1205
SQ SOURCE 1301 AA; 145336 MW; 8241E3E19A4CA5BD CRC64;

```

Query Match 34 8%; Score 469; DB 1; Length 1301;
 Best Local Similarity 37.7%; Pred. No. 4.7e-34; Index 24; Gaps 8;
 Matches 96; conservative 61; Mismatches 77;

```

QY 1 DPCGVAKIPKKNKRRHYDVSPPDHSHKIKH---QEDN-DY NASLAKMHAQRSYIL 55
Db 491 DLPCDSQHPENKRNKRYLNTLAYDHSVHLHPIGKKNLIDYINANFIDYKSHAFIG 550
QY 56 TQGLPRTCCIHPEVWVWVCKSGVAVLNPWEKFSGLKQAVQSEKEEEDFNLT 115
Db 551 TQGLPRTCCIHPEVWVWVCKSGVAVLNPWEKFSGLKQAVQSEKEEEDFNLT 115
QY 116 LISEDIKSYIV--LEENLTQETRE-----LIHFYTVWDFGVSPASFLNLFK 167
Db 607 LIEEVMSTYVTRKTLQIKLKKKCKCTEKLVAUYHYHNTMPDHGTDPHPLVINF-- 663
QY 168 VPPSSNSP--PQGVAVVHCAGIGRSCGFCIANICLIMKKNKVSVCIRKVLILMRKF 226
Db 664 VKRSSANANVEMGPIVWVSAGV--PTGTYIVLDMALFQYQK---NIVNVPFLRITPAQ 720
QY 227 FMGLTQATCLFSTYLAIV 246
Db 721 RMFLVQTFADYRFTYMAV 740

```

RESULT 14

• •

KC TISSUE-TYPE, AND REFERENCE: ASTOMA;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC008244; AAH08244.1;
 KW Receptor.
 SO SOURCE: 387 AA; 45168 MW; 0B3F622B8A5A92CH CIRC64;

Query Match 75.1%; Score 1011; DB 4; Length 387;
 Best Local Similarity 72.3%; Pred. No. 4e-87; 28; Indels 6; Gaps 3;
 Matches 185; Conservative 37; Mismatches 28;

QY 1 DPGGVAKIIPKKNRNRYNDVSPDHSRIKLIHQENDYINASLIIMPEAORSYLLTQGL 60
 DB 31 DPHRAKAFEPENPNRPRVPEVSPYHSRVLQNAENDYINASLVDEEORSYLLTQGL 90
 QY 61 PNTGHEWEMVFOKSGVVMINRYEKSGLKQVYFOKEKEKMEFEENIKLITISFD 120
 DB 91 PNTGHEWEMVFOKSGVVMINRYEKSGLKQVYFOKEKEKMEFEENIKLITISFD 149
 QY 121 IKSYIV--LELENTLTQETRELIHPHTTWPEEGVESPASFLNLFKVRSGSLSPEN 178
 DB 150 VKSYIVVHLQLENINSGLFRTSHFTYITWPEGVESPASFLNLFKVRSGSLSPEN 209
 QY 179 GPVAVHCSAGTSSGIFCTADTCLIMKPKPMSVSDIKKVLIMKPKPMQITGVAVH 248
 DB 210 GPVAVHCSAGTSSGIFCTADTCLIMKPKPMSVSDIKKVLIMKPKPMQITGVAVH 266
 QY 239 FSYAVIEGAKPIIMCD 254
 DB 267 FSYAVIEGAKPIIMCD 282

RESULT 5
 Q922E7 PRELIMINARY: 406 AA
 ID Q922E7
 AC Q922E7
 DT 01-DEC-2001 (TREMBLER: 19, Created)
 DT 01-DEC-2001 (TREMBLER: 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLER: 19, Last annotation update)
 DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX MBL:TaxID 10090.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC008269; AAH08269.1;
 KW Receptor.
 SO SOURCE: 406 AA; 47360 MW; DFB881DF3080DCC3 CIRC64;

Query Match 74.5%; Score 1008; DB 11; Length 406;
 Best Local Similarity 71.5%; Pred. No. 6.2e-87;
 Matches 183; Conservative 38; Mismatches 29; Indels 6; Gaps 3;

QY 1 DPGGVAKIIPKKNRNRYNDVSPDHSRIKLIHQENDYINASLIIMPEAORSYLLTQGL 60
 DB 31 DPHRAKAFEPENPNRPRVPEVSPYHSRVLQNAENDYINASLVDEEORSYLLTQGL 90
 QY 61 PNTGHEWEMVFOKSGVVMINRYEKSGLKQVYFOKEKEKMEFEENIKLITISFD 120
 DB 91 PNTGHEWEMVFOKSGVVMINRYEKSGLKQVYFOKEKEKMEFEENIKLITISFD 149
 QY 121 IKSYIV--LELENTLTQETRELIHPHTTWPEEGVESPASFLNLFKVRSGSLSPEN 178
 DB 150 VKSYIVVHLQLENINSGLFRTSHFTYITWPEGVESPASFLNLFKVRSGSLSPEN 209
 QY 179 GPVAVHCSAGTSSGIFCTADTCLIMKPKPMSVSDIKKVLIMKPKPMQITGVAVH 248
 DB 210 GPVAVHCSAGTSSGIFCTADTCLIMKPKPMSVSDIKKVLIMKPKPMQITGVAVH 266

QY 239 FSYAVIEGAKPIIMCD 254
 DB 267 FSYAVIEGAKPIIMCD 282

RESULT 6
 Q91BA4 PRELIMINARY: 322 AA.
 ID Q91BA4
 AC Q91BA4
 DT 01-OCT-2000 (TREMBLER: 15, Created)
 DT 01-OCT-2000 (TREMBLER: 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLER: 15, Last annotation update)
 DE KATP3A3 PROTEIN (FRAGMENT).
 OS Erythron.
 OC Potamogetron moloro (South American freshwater silurid).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squales; Hypnosquales; Pristigastera; Batoida;
 OC Myliobatiformes; Myliobatidae; Potamogetronidae; Potamogetron.
 OX NCBI_TaxID=86373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:20219325; PubMed:10754074;
 RA Ono-Koyanagi K., Suga H., Kato H., Miyata T.;
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
 KI divergence of tissue-specific isoform genes in the early evolution of
 vertebrates.";
 FL J. Mol. Evol. 50:302-311(2000).
 DR EMBL: AB033582; BAA95169.1;
 DR HSSP: P18031, 187J.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR006242; Tyr_Prot_Phosphatase.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPc; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase.
 FT NON_TER
 SO SOURCE: 322 AA; 36954 MW; B0045023E66F1197 CIRC64;

Query Match 54.9%; Score 739; DB 13; Length 322;
 Best Local Similarity 75.0%; Pred. No. 1.4e-61;
 Matches 148; Conservative 22; Mismatches 22; Indels 2; Gaps 1;

QY 73 EOKSKGVMLINRYEKSGLKQVYFOKEKEKMEFEENIKLITISFDIKSYIV--LELE 130
 DB 1 EOKSRAIVMLINRYEKSGLKQVYFOKEKEKMEFEENIKLITISFDIKSYIV--LELE 60
 QY 131 ENLTLQETRELIHPHTTWPEEGVESPASFLNLFKVRSGSLSPENHGVAVH 190
 DB 61 QRTSTGKREIYHHTTWPEEGVESPASFLNLFKVRSGSLSPENHGVAVH 120
 QY 191 KSGTFCIAGTCLIMKPKPMSVSDIKKVLIMKPKPMQITGVAVH 250
 DB 121 KSGTFCIAGTCLIMKPKPMSVSDIKKVLIMKPKPMQITGVAVH 180
 QY 251 LMD 254
 DB 181 LMD 184

RESULT 7
 Q9W0G1 PRELIMINARY: 548 AA.
 ID Q9W0G1
 AC Q9W0G1, Q9W0G2, Q97932;
 DT 01-MAY-2000 (TREMBLER: 13, Created)
 DT 01-MAY-2000 (TREMBLER: 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLER: 17, Last annotation update)
 DE PROTEIN-TYROSINE PHOSPHATASE 61F (FC 3.1.3.48) (PPP61F PROTEIN)
 DR (CG9181 PROTEIN).

RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.:
 "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
 RT divergence of tissue-specific isoform genes in the early evolution of
 vertebrates." J. Mol. Evol. 50:302-311(2000).

DR EMBL: AB034568; BAA95175.1; -
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR PRINTS: PR00700; PRYPPHPTASE.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase.
 FT NON_TER 1
 SQ SEQUENCE 331 AA; 38430 MW; 41A83A67D99FA59 CRC64;

Query Match 47.0%; Score 633; DB 5; Length 331;
 Host local similarity 62.0%; Pred. No. 1,46-51;
 Matches 116; Conservative 37; Mismatches 29; Indels 6; Gaps 2;

QY 73 FQKSGVYVNLNRYMKGSLKCAQYPOKE----EKEMFEDQNKLLISEDKSYTVL 128
 1 EORTKAVVNLNRYMKGSLKCAQYPOKE----EKEMFEDQNKLLISEDKSYTVL 60
 DB 61 TYLLOLKLTKNSKRYHPTITMPPGVESPAFLFLFLLEVRDSSLESDGPPVHCS 120
 QY 129 E--EHLTTCETPTTHPTWTPVCPSPASPI NPLFYVPSGSI SPBPGVNVHCS 186
 1 E--EHLTTCETPTTHPTWTPVCPSPASPI NPLFYVPSGSI SPBPGVNVHCS 186
 DB 187 ASIGRSSTFGLADFTLLMKRRKSSVDIKKVLLEMRFRKGLIOTADQLRSTLAVE 245
 121 AGIGRSGVCLVDCIYLDIKRHLISLIRPLIDMPQYPMGLIQTPQILRPSYLAIVR 180
 QY 247 GKRTMG 253
 DB 181 GAPTTLV 187

RESULT 9
 Q99TSL PRELIMINARY: PRT: 272 AA.
 AC Q99TSL: (ITEMBL:rel. 17, created)
 DT 01-JUN-2001 (ITEMBL:rel. 17, last sequence update)
 DT 01-JUN-2001 (ITEMBL:rel. 19, last annotation update)
 DE SIMILAR TO PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1
 DE (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBL:taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.:
 RL Submitted (AIR-2001) to the EMBL/GenBank/DBP databases
 DR EMBL: BC005729; AA045729.1; -
 DR HSSP: P18031; 2HNO.
 DR InterPro: IPR000387; PTPC; PTPC; 1.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRYPPHPTASE.
 DR SMART: SM00194; PTPC; 1.
 DR SMART: SM00404; PTPC_mol1; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase; Receptor.
 FT NON_TER 1
 SQ SEQUENCE 272 AA; 30630 MW; 430E25BP6494920 CRC64;

Query Match 45.9%; Score 631; DB 11; Length 272;
 Host local similarity 56.8%; Pred. No. 1,70-51;
 Matches 120; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 131 ENLITETREKELHHTTTPDPGVESPASFLNFKVPSGSLSPBPGVNVHCSAGIG 190
 1 ENLITETREKELHHTTTPDPGVESPASFLNFKVPSGSLSPBPGVNVHCSAGIG 60
 DB 191 RSCFTECLADITLMDKRRKDPSSVDIKKVLLEMRFRKGLIOTADQLRSTLAVE 250
 b1 RSCFTECLADITLMDKRRKDPSSVDIKKVLLEMRFRKGLIOTADQLRSTLAVE 120
 QY 251 IMGD 254
 DB 121 IMGD 124

RESULT 10
 Q9NKKZ PRELIMINARY: PRT: 379 AA.
 AC Q9NKKZ: (ITEMBL:rel. 15, created)
 DT 01-OCT-2000 (ITEMBL:rel. 15, last sequence update)
 DT 01-OCT-2000 (ITEMBL:rel. 19, last annotation update)
 DT 01-DEC-2001 (ITEMBL:rel. 19, last annotation update)
 DE HGFPN3 PROTEIN (FRAGMENT).
 CN HGFPN3.
 OS Epiplatys burgeri (Inshore hagfish).
 OC Eukaryota; Metazoa; Chordata; Clariata; Heterostei; Myxiniiformes;
 OC Myxiniidae; Epiplatinae; Epiplatini.
 OX NCBL:taxid=7764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 20124325; PubMed=10754074;
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.:
 "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
 RT divergence of tissue-specific isoform genes in the early evolution of
 vertebrates." J. Mol. Evol. 50:302-311(2000).

DR EMBL: AB033579; BAA95186.1; -
 DR HSSP: P18031; 2HNO.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRYPPHPTASE.
 DR SMART: SM00194; PTPC; 1.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase.
 FT NON_TER 1
 SQ SEQUENCE 379 AA; 42672 MW; A2493R3RFDQ0174 CRC64;

Query Match 43.7%; Score 588; DB 13; Length 379;
 Host local similarity 62.0%; Pred. No. 36-47;
 Matches 114; Conservative 26; Mismatches 38; Indels 6; Gaps 3;

QY 73 FQKSGVYVNLNRYMKGSLKCAQYPOKEKEKEMFEDQNKLLISEDKSYTV--LEL 130
 1 FQKSGVYVNLNRYMKGSLKCAQYPOKEKEKEMFEDQNKLLISEDKSYTV--LEL 59
 DB 131 ENLITETREKELHHTTTPDPGVESPASFLNFKVPSGSLSPBPGVNVHCSAGIG 190
 60 ECSTAKREVLHHTTTPDPGVESPASFLNFKVPSGSLSPBPGVNVHCSAGIG 119
 QY 191 RSCFTECLADITLMDKRRKDPSSVDIKKVLLEMRFRKGLIOTADQLRSTLAVE 250
 120 RSCFTECLADITLMDKRRKDPSSVDIKKVLLEMRFRKGLIOTADQLRSTLAVE 176
 QY 251 IMGD 254

us-09-788-626-2.01g.rag

Page 3

[illegible]

Matches 197: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GILPNTGCHFWEMWQKSGVYMLNRMFKSLKCAQYWPQKEEKEMLFEEDTNLKLTL 117
 58 qplntcghfwemwqksgvymlnrmfkslkcaqywpqkeekemlfedtnlkltl 117
 QY 118 SDPIKSYVLELELNLTDRELLPHHYTWDPGVPSFASFLNPLFKVRSGSLSPH 177
 118 sdplksyvlelelnltdrellphhytwdpvpsfaslfnplfkvrsgslsph 177
 QY 178 HGVVYVHCAGTSPSTFTLATCLLLMDKRRPSSVDIKKVLLEMRKFMGLIOTADOL 237
 178 hgvvyvhcagtspstftlatclllmdkrrpssvdiikkvlllemrkfmglilotadol 237
 QY 238 PFSYLAIECAKFTMD 254
 238 pfsylaviecakftmd 254
 DB 238 RSYLAIECAKFTMD 254

RESULT 3
 AAG78311
 ID AAG78311 standard; Protein: 321 AA.
 AC AAG78311;
 XX 20-NOV-2001 (first entry)
 DE human PTP1B mutant G215S catalytic domain (PTP1B/G215S).
 XX protein tyrosine phosphatase; PTP1B; catalytic domain; human;
 KW type II diabetes; obesity; inhibition; insulin signalling regulator;
 KM mutant; motilin.
 XX Homo sapiens.
 OS Synthetic.
 XX Key location/Qualifiers
 FT Misc-difference 215 /note- "Ser replaces wild type Cys"
 FT W0200164939-A2.
 FN 07-SEP-2001.
 PD 02-MAR-2001; 2001W0-EP0248
 PE 02-MAR-2001; 2001W0-EP0248
 PF 02-MAR-2001; 2000US-0517170.
 PR (MORF-) MORPHOCHRM AG.
 PA Liu Y, Wang S, Zhang Z.
 PI WPT: 2001-582165/65.
 DR N-PSDB: AAI64150
 XX Identifying inhibitors or activators of enzymes, particularly of
 PT protein tyrosine phosphatase for treating diabetes or obesity comprises
 PT using inactive, but substrate-binding enzyme mutant.
 XX Disclosure: page 7; 24pp; English.

CC and is easily adapted for high throughput screening.
 XX Sequence 321 AA:
 SQ 50.0%, Score 127, 38 22, Length 321;
 Query Match: Best Local Similarity 100.0%; Pctd. No. 5, 5e 121;
 Matches 127: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPCVAKLPKKNKRNKRVNSPTFHSKIKLHCEINDYINSLIKMEFQNSYITGSP 60
 1 depcvaklpkknkknrvnsptfhsiklhcendyinslikmefqnsyitgsp 60
 DB 29 dfervaklprkknunryldspfdhsrik;hgodyfnas;ikmeagpsy;itgsp 88
 29 dfervaklprkknunryldspfdhsrik;hgodyfnas;ikmeagpsy;itgsp 88
 QY 61 IPIICCHFWEMWQKSGVYMLNRMFKSLKCAQYWPQKEEKEMLFEEDTNLKLTL 120
 61 ipiicchfwemwqksgvymlnrmfkslkcaqywpqkeekemlfedtnlkltl 120
 DB 89 pteqnlwemwqksgvymlnrmfkslkcaqywpqkeekemlfedtnlkltl 148
 89 pteqnlwemwqksgvymlnrmfkslkcaqywpqkeekemlfedtnlkltl 148
 QY 121 IKSYYTV 127
 121 iksyytv 127
 DB 149 IKSYYTV 155

RESULT 4
 AAM48944
 ID AAM48944 standard; Protein: 323 AA.
 AC AAM48944;
 XX 26-OCT-1998 (first entry)
 DE Mutant human PTP1B tyrosine kinase phosphatase.
 XX Mutant human PTP1B tyrosine kinase phosphatase; PTP1B;
 KW scientific; insulin binding assay; diabetes; cancer;
 KM 4-phosphatase(difluoromethyl) phenylalanine group; osteoporosis.
 XX Homo sapiens.
 OS Synthetic.
 XX Key location/Qualifiers
 FT Misc-difference 323 /note- "The residue is encoded by GAC, but it is not specified in the specification which gives a 322 residue protein"
 FT Misc-difference 251 /note- "changed from Cys in wild type to Ser in mutant"
 FT W09820156-A1.
 FN 14-MAY-1998.
 PD 03-NOV-1997; 97WD-CAM0825.
 PE 04-NOV-1996; 96US-0030408.
 PR (MERI) MEPRK PROSST CANADA INC.
 PA Desmarais S, Ford-Hutchinson A, Friesen R, Gresser M;
 PI Kennedy B, Nicholson D, Ramchandran C, Skorey K;
 PT WPT: 1998-348103/30.
 XX Enzyme binding assay for detection of useful compounds - uses mutant
 FT form of wild-type enzyme, in which serine replaces cysteine at
 PT active site, to reduce interference from oxidising/alkylating agents
 XX Disclosure: pages 37-38, 63pp; English.
 CC The present sequence represents a mutated human PTP1B tyrosine kinase
 CC phosphatase. The protein has a truncation (comprising residues 1-320)
 CC and single point mutant (where residue 251 is changed from cysteine to
 CC serine) when compared to the wild type PTP1B tyrosine kinase phosphatase.

02-MAR-1990; 900S-0487733.
 (HIOF-) APPL BIOTECHN INC.
 Hruskin AM, Hill DE;
 WP1: 1991-281465/48.
 N-PSDB: AAN1643.
 Vector contg. protein phospho-tyrosyl phosphatase gene fragment
 for use in diagnosis of cancers, e.g. acute non-lymphocytic
 leukemia
 Claim 6: Fig 1: 73pp; English.
 A human placental cDNA library was screened with degenerate probes
 deduced from the partial amino acid sequence of the pPase 1B (see
 AAO13653 and AAO13654 for probe sequences). One recombinant
 bacteriophage hybridised to both probes and was shown to contain a
 3.2 kb fragment. The fragment was subcloned in pEMV2 and sequenced.
 The open reading frame was predicted to encode this 435 amino acid
 protein. The calculated mol wt is 49,966. pPase 1B is useful for
 treatment of AML, myelodysplastic syndrome and myeloproliferative
 disorders. See also AAO13644-Q13654.

Sequence 435 AA:

Query Match 50.0%; Score 127; DB 12; Length 435;
 Best Local Similarity 100.0%; Freq. No. 7, 2e-121;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPCVAKLPKNNKNNRYPVSPPHSRIRIKLHEDNDYINASTLKMPFAOSYILLTGPL 60
 29 dpcrvaklpknknrryrvspphsrirkhgedndyinaslkmpcagysylltgpl 88
 DB 61 PNTGHHWEMWEMKSGVYVMLNPKWMEKSLKCAQVWPQKEKEMIFEDNLKLTLISEG 120
 89 pntgghwemwemksgvymlnpkwmekslkcaqwpqkeekemifednlkltlised 148
 QY 121 IKSYIIV 127
 149 lksyyiv 155
 DB

RESULT 7

AAM51203
 ID AAM51203 standard; Protein: 435 AA.

AC AAM51203;

DI 19-DEC-2001 (first entry)

DE Human PTP1B mutant D181A.

PTP: protein tyrosine phosphatase, tyrosine phosphorylated polypeptide;
 dephosphorylation; phosphotyrosine; human; PTP1B; mutant; mutant.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FI Mismatch 181 /note- "Wild-type Asp substituted by Ala"

PD W0200161031-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US05180

PR 14-FEB-2000; 2000US-0181769.

XX

PA (CEPT-) CEPTK INC.
 XX
 PI Plint AJ, Cool DE;
 XX
 DX WP1: 2001-570570/64.

PT Screening assays to identify agents that alter protein tyrosine
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic
 PT dephosphorylation of phosphotyrosine peptide substrates

XX Example 1; Page -: 79pp; English.

XX The invention relates to identifying agents which alter the interaction
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine
 CC phosphorylated polypeptide using fluorescence energy signals. The methods
 CC are useful for performing screening assay to identify agents that alter
 CC PTP binding to and PTP mediated catalytic dephosphorylation of
 CC phosphotyrosine peptide substrates. The present sequence is that of a
 CC human PTP1B D181A mutant.
 CC Note: The present sequence is not given in the specification but is
 CC derived from the wildtype human PTP1B sequence (AAM51206) from
 CC Genbank (Accession Number: U18031). An alternative sequence for human
 CC PTP1B is given in figure 1 of the specification (AAC78262).

XX Sequence 435 AA:

Query Match 50.0%; Score 127; DB 22; Length 435;
 Best Local Similarity 100.0%; Freq. No. 7, 2e-121;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPCVAKLPKNNKNNRYPVSPPHSRIRIKLHEDNDYINASTLKMPFAOSYILLTGPL 60
 29 dpcrvaklpknknrryrvspphsrirkhgedndyinaslkmpcagysylltgpl 88
 DB 61 PNTGHHWEMWEMKSGVYVMLNPKWMEKSLKCAQVWPQKEKEMIFEDNLKLTLISEG 120
 89 pntgghwemwemksgvymlnpkwmekslkcaqwpqkeekemifednlkltlised 148
 QY 121 IKSYIIV 127
 149 lksyyiv 155
 DB

RESULT 8

AAM51204
 ID AAM51204 standard; Protein: 435 AA.

AC AAM51204;

DI 19-DEC-2001 (first entry)

DE Human PTP1B mutant C215S.

PTP: protein tyrosine phosphatase, tyrosine phosphorylated polypeptide;
 dephosphorylation; phosphotyrosine; human; PTP1B; mutant; mutant

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FI Mismatch 215 /note- "Wild-type Cys substituted by Ser"

PD W0200161031-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US05180.

PR 14-FEB-2000; 2000US-0181769.

XX (CEPT-) CEPTK INC.

```

XX      Eland AL, Oost DB;
XX      W01: 2001 5/05/04/4
XX
XX      Screening assays to identify agents that alter protein tyrosine
XX      phosphorylation (PTP) binding to, and PTP mediated catalytic
XX      phosphorylation of phosphotyrosine peptide substrates
XX
XX      Example 1: Page 7: 7pp: English.
XX
XX      The invention relates to identifying agents which alter the interaction
XX      between a protein tyrosine phosphatase (PTP) and a tyrosine
XX      phosphorylated polypeptide using fluorescence energy signals. The methods
XX      are useful for performing screening assay to identify agents that alter
XX      PTP binding to and PTP mediated catalytic dephosphorylation of
XX      phosphotyrosine peptide substrates. The present sequence is that of a
XX      human PTP1B c215s mutant.
XX      Note: The present sequence is not given in the specification but is
XX      derived from the wild-type human PTP1B sequence (AA051206) from
XX      Genbank (Accession Number: P18031). An alternative sequence for human
XX      PTP1B is given in Figure 1 of the specification (AA078262).
XX
XX      Sequence 435 AA:
XX
XX      Query Match          50.0%; Score 127; DB 22; Length 435;
XX      Best local Similarity 100.0%; Pred. No. 7.2e-121;
XX      Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 DFGYVAKLPRKNNRKYRVSFEDSRIRKIQEDNDYINASLIKMEEAQRSYLTGQPL 60
XX      I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX      29 dfgvraakprvnnrnygdsfpdssrikhgsndyfnaslrkccagfsytltgqpl 88
XX
XX      61 PNTGHEFKRWVEQKSNVVMINPWEKRSIKCAAYWPKFFEREMIEETINRILISED 120
XX      I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX      89 pntgblwewwvqsgsyvmfnrwmeksklkcaiywpkfkkemilfoqlklilised 148
XX
XX      121 IKSYYIV 27
XX      I I I I I I
XX      149 IKSYYIV 155
XX
XX      RESULT 10
XX      AA051206
XX      ID AA051206 standard; Protein: 435 AA.
XX
XX      AC AA051206;
XX
XX      DE 1-6pp: 2001 (first entry)
XX
XX      Human protein Genbank Accession Number P18031.
XX
XX      PTP: protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
XX      dephosphorylation; phosphotyrosine; human; PTP1B.
XX
XX      Homo sapiens.
XX
XX      W0200610031 A2;
XX
XX      24 A01: 2001.
XX
XX      14 PTP 2001: 2001w: 0505180.
XX
XX      14 PTP 2000: 2000US 0 012-9.
XX
XX      (CEBT ) CEBTYR INC.
XX
XX      Eland AL, Oost DB;
XX      W01: 2001 5/05/04/4.
XX
XX      Screening assays to identify agents that alter protein tyrosine

```

```

XX      Phosphatase (PTP) binding to, and PTP mediated catalytic
XX      dephosphorylation of phosphotyrosine peptide substrates
XX
XX      Example 1: Page 7: 7pp: English.
XX
XX      The invention relates to identifying agents which alter the interaction
XX      between a protein tyrosine phosphatase (PTP) and a tyrosine
XX      phosphorylated polypeptide using fluorescence energy signals. The methods
XX      are useful for performing screening assay to identify agents that alter
XX      PTP binding to and PTP mediated catalytic dephosphorylation of
XX      phosphotyrosine peptide substrates. The present sequence is not given in
XX      the specification but is that of human PTP1B protein sequence taken from
XX      Genbank (Accession Number: P18031). The present sequence was used to
XX      generate mutants D18A (AA051203) and c215S (AA051204) as described in
XX      the specification.
XX      Note: An alternative sequence for human PTP1B is given in Figure 1 of
XX      the specification (AA078262).
XX
XX      Sequence 435 AA:
XX
XX      Query Match          50.0%; Score 127; DB 22; Length 435;
XX      Best local Similarity 100.0%; Pred. No. 7.2e-121;
XX      Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 DFGYVAKLPRKNNRKYRVSFEDSRIRKIQEDNDYINASLIKMEEAQRSYLTGQPL 60
XX      I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX      29 dfgvraakprvnnrnygdsfpdssrikhgsndyfnaslrkccagfsytltgqpl 88
XX
XX      61 PNTGHEFKRWVEQKSNVVMINPWEKRSIKCAAYWPKFFEREMIEETINRILISED 120
XX      I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX      89 pntgblwewwvqsgsyvmfnrwmeksklkcaiywpkfkkemilfoqlklilised 148
XX
XX      121 IKSYYIV 127
XX      I I I I I I
XX      149 IKSYYIV 155
XX
XX      RESULT 10
XX      AA05848
XX      ID AA05848 standard; Protein: 435 AA.
XX
XX      AC AA05848;
XX
XX      DE 25-Sep-2001 (first entry)
XX
XX      Human protein phosphatase 1B (PTP1B).
XX
XX      Human; protein phosphatase 1B; PTP1B; antisense; gene therapy;
XX      infection; inflammation; tumour; prophylaxis.
XX
XX      Homo sapiens.
XX
XX      OS US6261840-D1.
XX
XX      PD 17-JUL-2001.
XX
XX      18-JAN-2000; 2000US-0487368.
XX
XX      18-JAN-2000; 2000US-0487368.
XX
XX      (ISIS ) ISIS PHARM INC.
XX
XX      Cowsort LM, Wyatt J;
XX
XX      WPI: 2001-432181/46.
XX      N-PSDB: ADL1946.
XX
XX      New antisense compounds capable of modulating expression of human
XX      protein phosphatase 1B, useful for diagnosis, prophylaxis and treatment
XX      of diseases associated with expression of protein phosphatase
XX
XX      Example 14; Column 55-60; 71pp: English.

```


used as a local additive or preservative to increase storage capabilities. Sequences AM60016, 200024 and AM64453 are used in the course of the invention during the identification and characterisation of the protein and nucleotide sequences.

Sequence 59 AA:

Query Match 20 90% Score 54; DB 21; Length 59;
Best Local Similarity 100.0%; Pred. No. 4,1e-46;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

59 YINASTLKPEFAKSYILTQGLPNTGHEFEMVWEEKSGEVMILNRYEKGS 90
|||||
14 YINASTLKPEFAKSYILTQGLPNTGHEFEMVWEEKSGEVMILNRYEKGS 53

RESULT 14

AM62813

ID AM62813 standard; Protein; 498 AA.

XX

XX

19 FEB 2002 (first entry)

Mouse human diaphosyl protein #28519.

Human chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Human sapiens.

W0200175067 A2.

11 OCT 2001.

60 MAR 2001; 2001W010308641.

41 MAR 2001; 2001W010308641.

24 AUG 2000; 2000US 0049467.

(HYTE) HY350 (M).

Human RT, L10 Y, Lang Y1.

W01; 2001 609862714.

N 15308; AAS647 Dc.

New isolated polynucleotide and encoded polypeptides; useful in diagnosis; forensic; gene mapping; identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID No 54878; 10pp; English.

The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polynucleotide chain reaction (PCR) primers, oligomers, and for chromosomal and gene mapping, and in recombinant production of (11). The polynucleotide are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques for restoring normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in diagnosis, forensic, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AM60016, AM60024 and AM64453 represent novel human diaphosyl protein and sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pat/published_pat_sequences.

Sequence 498 AA:

Query Match 14 0% Score 33; DB 22; Length 498;
Best Local Similarity 100.0%; Pred. No. 4.9e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GPLPNTGHEFEMVWEEKSGEVMILNRYEKGS 90
|||||
Db 309 GPLPNTGHEFEMVWEEKSGEVMILNRYEKGS 341

RESULT 14

AAG78263

ID AAG78263 standard; Protein; 251 AA.

XX

XX

19 DEC 2001 (first entry)

Human TCEPT.

PPP: protein tyrosine phosphatase; tyrosine phosphorylated polypeptide; dephosphorylation; phosphotyrosine; human; PTHB; mouse; fruit fly; yeast.

Human sapiens.

W0200161031 A2.

23 AUG 2001.

13 FEB 2001; 2001W010505180.

14 FEB 2000; 2000US 0181769.

(CEPT) CEPTOR INC.

Flint AL, Cool DE;

W01; 2001-570570/64.

Screening assays to identify agents that alter protein tyrosine phosphatase (PTP) binding to, and PTP mediated catalytic dephosphorylation of phosphotyrosine peptide substrates.

Disclosure; Fig 1; 7pp; English.

The invention relates to identifying agents which alter the interaction between a protein tyrosine phosphatase (PTP) and a tyrosine phosphorylated polypeptide using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter PTP binding to and PTP mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is that of a catalytic domain of a PTP for comparison with human PTPB (AAG78262).

Sequence 251 AA:

Query Match 12 5% Score 32; DB 22; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.8e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 HEFTWPEFVPEPASELNFKEVRESST 174
|||||
Db 141 HFTWPEFVPEPASELNFKEVRESST 172

RESULT 15

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run On: June 18, 2002, 15:00:15 Search time 19.23 seconds
(without alignments)
1294 Iva M11100 v-11 updates/sec

Title: US-09-788-626-2

Perfect score: 254
Sequence: 1 DEPCNVALIKKNNPPYPD DQLEPSYLAIVGAKFIMSD 254

Scoring table: Gapop 60.0, Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size: 0 283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: 1: FIR-7114
2: PIR1
3: PIR2
4: PIR3
5: PIR4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	50.0	435	1	TPHUN1
2	78	30.7	432	1	A34845
3	64	25.2	432	1	IN0317
4	55	21.7	356	2	JM0049
5	32	12.6	363	1	S14294
6	32	12.6	387	1	A60345
7	32	12.6	415	1	A33899
8	30	11.8	382	1	A38191
9	16	6.3	535	2	A46101
10	16	6.3	548	2	B46101
11	14	5.5	377	1	A48711
12	13	5.1	347	2	S53427
13	13	5.1	585	2	A52004
14	13	5.1	593	2	JN0805
15	13	5.1	593	2	JN5167
16	13	5.1	595	1	A55651
17	13	5.1	597	1	A53593
18	13	5.1	656	1	A55574
19	13	5.1	656	1	JC1263
20	12	4.7	694	2	A53978
21	12	4.7	926	2	A41105
22	11	4.3	2294	2	S71626
23	11	4.3	2458	2	S71626
24	11	4.3	2466	2	S71626
25	11	4.3	2490	2	A54971
26	10	3.9	135	2	H88683
27	10	3.9	250	2	A40169
28	10	3.9	352	2	T06536
29	10	3.9	344	2	T12869

30	10	3.9	352	2	T20729	hypothetical prote
31	10	3.9	360	1	JH0692	protein-tyrosine-p
32	10	3.9	365	2	T25917	hypothetical prote
33	10	3.9	374	2	F88712	protein C17H12.3
34	10	3.9	398	2	T16540	protein-tyrosine-p
35	10	3.9	398	2	T33446	hypothetical prote
36	10	3.9	398	2	T08716	protein-tyrosine-p
37	10	3.9	593	1	A42690	protein-tyrosine-p
38	10	3.9	597	2	B53978	hypothetical prote
39	10	3.9	597	2	T21883	hypothetical prote
40	10	3.9	621	2	T21090	hypothetical prote
41	10	3.9	624	2	T19630	hypothetical prote
42	10	3.9	668	2	T134317	probable protein
43	10	3.9	1026	2	T19631	hypothetical prote
44	10	3.9	1156	2	T23308	hypothetical prote
45	10	3.9	1262	1	B48758	protein-tyrosine-p

ALIGNMENTS

RESULT 1
TPHUN1
protein-tyrosine phosphatase (EC 3.1.3.48), nonreceptor type 1 [validated] - human
N:Alternate names: phosphotyrosine phosphatase JB, long form; protein-tyrosine phosphatase JB, long form; protein-tyrosine phosphatase JB, long form; membrane-bound form; pr
N:Contains: protein-tyrosine phosphatase, nonreceptor type 1, membrane-bound form; pr
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence, revision 07-Apr-1994 #text, change 15-Sep-2000
C:Accession: A35992; 159169; 179576; S15849; A33897; A37275
R:Chernoff, J.; Schievella, A.R.; Joshi, C.A.; Erikson, R.L.; Neel, B.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 2735-2739, 1990
A:Title: Cloning of a cDNA for a major human protein-tyrosine phosphatase.
A:Reference number: A35992; M01D:30207272
A:Accession: A35992
A:Molecule type: mRNA
A:Residues: 1-435 <CHP>
A:Cross-references: GB:M1724; NIH:q190741; EMBL:AAA6023.1; PIR:q190742
R:Brown-Shiner, S.; Johnson, K.A.; Lawrence, J.B.; Johnson, G.; Brunkin, A.; Green, N
Proc. Natl. Acad. Sci. U.S.A. 87, 5148-5152, 1990
A:Title: Molecular cloning and chromosome mapping of the human gene encoding protein
A:Reference number: 159169; M01D:90311360
A:Accession: 159169
A:Status: translated from GB/EMBL/DBJ
A:Title: Purification and characterization of a higher-molecular mass form of protein
A:Reference number: S15849; M01D:91264781
A:Accession: S15849
A:Molecule type: protein
A:Residues: 1-435 <CHP>
R:Charbonneau, H.; Tonks, N.K.; Kumar, S.; Hanks, C.D.; Harrylock, M.; Cool, D.E.; AT
Proc. Natl. Acad. Sci. U.S.A. 86, 5252-5256, 1989
A:Title: Human placenta protein-tyrosine phosphatase: amino acid sequence and relation
A:Reference number: A33897; M01D:89315775
A:Accession: A33897
A:Molecule type: protein
A:Residues: 1-321 <CHAS>
R:Barford, D.; Flint, A.J.; Tonks, N.K.
Submitted to the Brookhaven Protein Data Bank, September 1994
A:Contents: annotation; X-ray crystallography, 2.8 angstroms; residues 5-282
R:Barford, D.; Flint, A.J.; Tonks, N.K.
Science 263, 1397-1404, 1994
A:Title: Crystal structure of human protein-tyrosine phosphatase JB.
A:Reference number: A38904; M01D:94174273

RESULT 4
JW0049

protein-tyrosine-phosphatase (p65, 5,1,3,46) 1 chicken
 C1Species gallus gallus (chicken)
 C1Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 03-Dec-1995

Accession: JWO049
 R: Jung, E.J., Kang, Y.S., Kim, C.W.

Biochem. Res. Commun. 246, 238-242, 1998
Title: Multiple phosphorylation of chicken protein tyrosine phosphatase 1 and human PTPN49
Reference number: JWB049; MIMP-02262948

A:Accession: J20049
A:Molecule type: mRNA

A-Residues: 1356 (cont.)
C-Superfamily: protein-tyrosine-phosphatase, receptor type 1, protein-tyrosine-phosphatase, phosphotyrosine phosphatase hydrolyase

Cytosolic phospholipase A₂ (cPLA₂) is a member of the phospholipase A₂ family of enzymes that hydrolyze membrane phospholipids to release arachidonic acid, a precursor of eicosanoids. cPLA₂ is a calcium-dependent enzyme that is activated by a variety of stimuli, including growth factors, hormones, and neurotransmitters. The activation of cPLA₂ is a complex process involving the phosphorylation of the enzyme at two distinct sites. The first site is a serine residue (Ser505) that is phosphorylated by a serine kinase (PKC) in response to the binding of a ligand to a G-protein-coupled receptor (GPCR). The second site is a tyrosine residue (Tyr68) that is phosphorylated by a tyrosine kinase (Src) in response to the binding of a ligand to a receptor tyrosine kinase (RTK). The phosphorylation of both sites is required for the full activation of cPLA₂. The activated cPLA₂ then hydrolyzes membrane phospholipids to release arachidonic acid, which is then converted to eicosanoids by cyclooxygenase (COX) and lipoxygenase (LOX) enzymes. Eicosanoids are signaling molecules that regulate a variety of cellular processes, including inflammation, cell growth, and differentiation.

Keywords: Alternative splicing; phosphoprotein; phosphatase; monomer; hydrolyase; tyrosine
 EC: 2.4.4/kinase; protein-tyrosine-phosphatase homology <PTP>
 EC: 2.4.4/active site; Cys (phosphocysteine intermediate) *status predicted
 EC: 2.2/Binding site; substrate phosphate (Arg) *status predicted

Query Match 12.98% Score 327 DB 1: Length 4157
 Best Local Similarity 100.00% Pred. No. 6,482,243
 Matches 427 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

14 HHHV11WPGVVFVSSVSTNLEPKVRSGL 174
 114 HHHV11WPGVVFVSSVSTNLEPKVRSGL 205

RESULT 8
 A:Accession: A46191

protein-tyrosine phosphatase (EC 2.4.4.48) 11A - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 12 Feb 1994 #sequence_revision 02-May-1994 #text_change 11 Jun-1999

C:Accession: A46191
 R:McLaughlin, S.; Dixon, J.R.; Tremblay, H.; Tremblay, M.L.

A:Title: Cloning and characterization of a mouse cDNA encoding a cytoplasmic protein-tyr

A:Reference number: A46191; M01D:92115688

A:Accession: A46191

A:Accession: Type: mRNA

A:Cross-references: GI: 10423605

A:Note: sequence extracted from N91 cDNA library (NCBI:75899, M01P:75812)

C:Comment: This transcript was found in a variety of embryonic and adult tissues. A short

C:Keywords: alternative splicing; phosphoprotein; phosphatase; monomer; hydrolyase; tyros

EC: 2.4.4/kinase; protein-tyrosine-phosphatase homology <PTP>
 EC: 2.2/Binding site; Cys (phosphocysteine intermediate) *status predicted

Query Match 11.88% Score 301 DB 1: Length 4827
 Best Local Similarity 100.00% Pred. No. 5,282,213
 Matches 402 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

14 HHHV11WPGVVFVSSVSTNLEPKVRSGL 172
 114 HHHV11WPGVVFVSSVSTNLEPKVRSGL 203

RESULT 9
 A:Accession: A46191

protein-tyrosine phosphatase (EC 2.4.4.48) nonreceptor type PTPase; short splice form

C:Species: Drosophila melanogaster
 C:Date: 02 May 1995 #sequence_revision 12 May 1995 #text_change 22 Jun-1999

C:Accession: A46191
 R:McLaughlin, S.; Dixon, J.R.

A:Title: Alternative splicing gives rise to a nuclear protein-tyrosine phosphatase in D

A:Reference number: A46191; M01D:92115687

A:Accession: A46191

A:Accession: Type: mRNA

A:Cross-references: GI: 10423605

A:Note: authors translated the cDNA for the protein residue 482 as Ile, and CAA for residue 528

Query Match 6.38% Score 163 DB 2: Length 5457
 Best Local Similarity 100.00% Pred. No. 2,582,073
 Matches 163 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

182 VVHSCAGIGRSGTCL 197
 234 VVHSCAGIGRSGTCL 249

RESULT 10
 A:Accession: A46101

protein-tyrosine phosphatase (EC 2.4.4.48), nonreceptor type PTPase; long splice form

C:Species: Drosophila melanogaster
 C:Date: 08 May 1995 #sequence_revision 12 May 1995 #text_change 24 Apr-1998

C:Accession: A46101
 R:McLaughlin, S.; Dixon, J.R.

A:Title: Alternative splicing gives rise to a nuclear protein-tyrosine phosphatase in

A:Reference number: A46101; M01D:92115607

A:Accession: A46101

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-548 <MOL>

A:Cross-references: GI: 111251

A:Note: authors translated the cDNA for residue 482 as Ile

C:Genetics:

A:Gene: PTPase

A:Cross-references: PTPase: PTPase

C:Species: Drosophila melanogaster

C:Keywords: alternative splicing; phosphoprotein; phosphatase; monomer; hydrolyase; tyr

EC: 2.4.4/kinase; protein-tyrosine-phosphatase homology <PTP>
 EC: 2.2/Binding site; Cys (phosphocysteine intermediate) *status predicted

EC: 2.2/Binding site; substrate phosphate (Arg) *status predicted

Query Match 6.38% Score 163 DB 2: Length 5457
 Best Local Similarity 100.00% Pred. No. 2,582,073
 Matches 163 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

182 VVHSCAGIGRSGTCL 197
 234 VVHSCAGIGRSGTCL 249

RESULT 11
 A:Accession: A46101

protein-tyrosine phosphatase (EC 2.4.4.48), nonreceptor type 2 - slime mold (Dictyost

N:Alternate names: protein-tyrosine-phosphatase DdbTpa; PTP2

C:Species: Dictyostelium discoideum

C:Date: 02 Jun 1995 #sequence_revision 08 Mar 1996 #text_change 11 Jun-1999

C:Accession: A46101; A53774

R:McLaughlin, S.; Shaw, D.R.; Emms, H.L.

A:Title: Cloning and functional expression of a Dictyostelium discoideum protein tyro

A:Reference number: A46101; M01D:9403028

A:Accession: A46101

A:Accession: Type: mRNA

A:Residues: 1-477 <RAM>

A:Cross-references: GI: 115420; NID:929036; PIR:AAA42422.1; PIR:429037

R:McLaughlin, S.; Shaw, D.R.; Emms, H.L.

A:Title: Cloning and functional expression of a Dictyostelium discoideum protein tyro

A:Reference number: A53774; M01D:94030645

A:Accession: A53774

A:Status: nucleotide sequence not shown

A:Molecule type: DNA

A:Residues: 1-477 <RAM>

A:Cross-references: GI: 115420; NID:929036; PIR:AAA42422.1; PIR:429037

A:Note: the translation of the nucleotide sequence is not complete in this paper

C:Species: Dictyostelium discoideum

C:Keywords: phosphoprotein; phosphatase; monomer; hydrolyase; tyrosine-specific phosph

EC: 2.4.4/kinase; protein-tyrosine-phosphatase homology <PTP>
 EC: 2.2/Binding site; Cys (phosphocysteine intermediate) *status predicted

E2.6.100/bovine SH2 homology - SH2A
 E2.11.2.214/bovine SH2 homology - SH2B
 E2.27.3.510/bovine protein tyrosine phosphatase homolog - PTP
 E2.45.4/bovine sites (phosphotyrosine intermediate) #status predicted
 E2.46.5/bovine sites substrate phosphate (ATP) #status predicted

Query Match

%ID# Score 14: DB 1: Length 5943

Best local similarity: 100.0%: Fred. No.: 0.000227

Matches: 14: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 159 GVVVHSA:108 197

LD 453 GVVVHSA:108 463

RESULT 15

P5167

Protein Tyrosine Phosphatase (P5167, 4.1.4.48), nonreceptor type 11 - chicken
 N.A. (chicken) names: phosphotyrosine phosphatase; ptp1b; ptp2c; SH-PTP2; syp
 (Species: Gallus gallus (chicken))

Collected: 21 Feb 1997 #sequence revision 27 Feb 1997 #text change 16 Jul 1999

Accession: J05167

RefSeq: J05167; LaMontagne, K.R.; Links, N.K.; Hayman, M.J.

Gene: PTP, 93,927, 1996

Active cloning and expression of the chicken protein tyrosine phosphatase SH-PTP2.

Accession number: J05167; MIM:197080906

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Accession: J05167

Search completed: June 18, 2002, 15:00:43

Job time: 28 sec

Query Match

%ID# Score 14: DB 2: Length 5943

Best local similarity: 100.0%: Fred. No.: 0.000227

Matches: 14: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 159 GVVVHSA:108 197

LD 453 GVVVHSA:108 463

E2.11.2.214/bovine SH2 homology - SH2A

E2.27.3.510/bovine protein tyrosine phosphatase homolog - PTPs

E2.45.4/bovine sites (phosphotyrosine intermediate) #status predicted

E2.46.5/bovine sites substrate phosphate (ATP) #status predicted

E2.46.5/bovine sites substrate phosphate (ATP) #status predicted

Gencore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 15:00:15 ; Search time 11.07 seconds
(without alignments)

888.416 Million cell updates/sec

Title: us-09-788-626-2

Perfect score: 254

Sequence: 1 DFGPRVAKLPRKNPNPNP

DQRFSTLVAVESAKTIMGD 254

Scoring table: 0.160

Gapop 60.0 ; Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	50.0	435	1	PTN1_HUMAN
2	79	31.1	432	1	PTN1_MOUSE
3	78	30.7	432	1	PTN1_RAT
4	56	22.0	434	1	PTN1_CHICK
5	32	12.6	363	1	PTN2_RAT
6	32	12.6	415	1	PTN2_HUMAN
7	30	11.8	377	1	PTN2_MOUSE
8	14	5.1	377	1	PTN2_DICDI
9	14	5.1	585	1	PTN3_MOUSE
10	13	5.1	593	1	PTN3_HUMAN
11	13	5.1	543	1	PTN3_RAT
12	13	5.1	989	1	PTN3_DICDI
13	12	4.7	926	1	PTN4_HUMAN
14	11	4.3	2485	1	PTN4_HUMAN
15	10	3.9	360	1	PTN7_RAT
16	10	3.9	593	1	PTN7_HUMAN
17	10	3.9	1026	1	PTN9_HUMAN
18	10	3.9	1422	1	PTN9_MOUSE
19	10	3.9	2314	1	PTN9_CHICK
20	10	3.9	2314	1	PTN9_HUMAN
21	10	3.9	2314	1	PTN9_FAT
22	10	3.9	363	1	PTN5_FAT
23	9	3.5	537	1	PTN5_HUMAN
24	9	3.5	541	1	PTN5_MOUSE
25	9	3.5	541	1	PTN5_HUMAN
26	9	3.5	595	1	PTN6_MOUSE
27	9	3.5	845	1	PTN6_MOUSE
28	9	3.5	913	1	PTN3_HUMAN
29	9	3.5	1630	1	PTN1_MOUSE
30	8	3.1	521	1	PTN1_MOUSE
31	8	3.1	1238	1	PTN1_MOUSE
32	8	3.1	1337	1	PTN1_MOUSE
33	7	2.8	109	1	PTN4_STYPL

34	7	2.8	110	1	PTN3_STYPL
35	7	2.8	116	1	PTN3_STYPL
36	7	2.8	151	1	SP2C_STYPL
37	7	2.8	194	1	HIS7_MOUSE
38	7	2.8	332	1	THPA_HAEN
39	7	2.8	335	1	PTN1_YEAST
40	7	2.8	417	1	ASP_MOUSE
41	7	2.8	501	1	CRP5_MOUSE
42	7	2.8	507	1	GAG_STYPL
43	7	2.8	699	1	PTN6_MOUSE
44	7	2.8	700	1	PTN6_HUMAN
45	7	2.8	796	1	PTN4_FAT

ALIGNED

RESULT	1	STANDARD	PRT	435 AA
PTN1_HUMAN				
ID	PTN1_HUMAN			
AC	P18031; Q9NQ04; Q9H0V9;			
DT	01-NOV-1990 (Ref. 16, Created)			
DT	01-NOV-1990 (Ref. 16, Last sequence update)			
DT	01-MAR-2002 (Ref. 41, Last annotation update)			
DE	Protein-tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48)			
DE	(Protein-tyrosine phosphatase 1b) (PTP-1b).			
CN	PTN1 OR PTP1B.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N A			
RC	TISSUE=Placenta;			
KX	MDLINE=90207272; PubMed=2157211;			
RA	Chernoff J., Schiewella A.R., Jost C.A., Erikson R.L., Neel B.G.;			
PT	"Cloning of a cDNA for a major human protein-tyrosine phosphatase."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2745-2749(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
KX	MEDLINE=9011163; PubMed=2164324;			
RA	Brown-Shamer S., Johnson K.A., Lawrence J.B., Johnson C.;			
RT	Broskin A., Green N.R., Hill D.E.;			
RT	"Molecular cloning and chromosome mapping of the human gene encoding			
EL	protein phosphotyrosyl phosphatase 1b." (1990).			
EL	Proc. Natl. Acad. Sci. U.S.A. 87:5148-5152(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	DeJouk P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.;			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Hagley C.L.;			
RA	Bailey J., Bartow K.F., Bates K.N., Heald L.M., Heare D.M.;			
RA	Bosley O.F., Bird C.P., Blakely S.F., Bridgman A.M., Brown A.J.;			
RA	Buck D., Burdill W., Butler A.P., Garder C., Garner N.P.;			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.;			
RA	Clegg S., Copley V.E., Collier R.E., Doherty R., Gaby N.R.;			
RA	Conlon A., Coville G.J., Deaman R., Dhani P., Dunn M.;			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.;			
RA	Griffiths M.N.D., Griffiths M.N.D., Griffiths M.N.D., Hall R.R.;			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.T.;			
RA	Huckle E., Hunt A.P., Hunt S.E., Jekesch K., Johnson G.M., Johnson D.;			
RA	Kay M.P., Kimberley A., King A., Knights A., Laird G.K., Lawlor S.;			
RA	Lehvaslahti M.H., Leverisha M., Lloyd G., Lloyd D.M., Lovell J.D.;			
RA	Marsh V.L., Martin S.L., McComacchie L., Mealy K., Murray A.A.;			
RA	Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.;			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.;			
RA	Phillimore R.T.F., Prathalingam S.R., Plumb R.W., Ramsay H.;			
RA	Rice C.M., Ross M.T., Scott C.E., Serna H.K., Snowken K., Sims S.;			
RA	Syme G.P., Smith M.L., Soderlund C., Steward C.A., Sulston J.R.;			
RA	Swann M., Syme N., Taylor R., Tye L., Thomas D.W., Thorpe A.;			
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.;			
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.;			
RA	Wilming L., Wray F.W., Hubbard T., Dublin P.M., Bentley D.F., Beck S.;			

GN PTPN1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis.
 RX MEDLINE=92328784; PubMed 1378268;
 RA Miyasaka H., Li S.S.L.
 RT "The cDNA cloning, nucleotide sequence and expression of an
 RL intracellular protein tyrosine phosphatase from mouse testis."
 RN Biochem. Biophys. Res. Commun. 185:818-825(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liao K., Lane M.D.
 RN Submitted (Apr-1995) to the EMBL/Genbank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain.
 RA Park K., Hyun S.
 RN Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 102-213 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain.
 RX MEDLINE=95134232; PubMed 7832766;
 RA Hendriks W., Schepens J., Houtman G., Zecunen P., Wieringa B.
 RT "A novel receptor-type protein tyrosine phosphatase with a single
 RL catalytic domain is specifically expressed in mouse brain."
 RN Biochem. J. 305:499-504(1995).
 RN [5]
 RP SEQUENCE OF 161-432 FROM N.A.
 RA Strassberg R.
 RN Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O -> protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA
 CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS
 CC THE CYTOSOL (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN TESTIS. ALSO FOUND IN KIDNEY,
 CC SPLEEN, MUSCLE, LIVER, HEART AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M97590; - NOT ANNOTATED CDS.
 DR EMBL: LA0595; AAA64615.1; -
 DR EMBL: U24700; AA98605.1; -
 DR EMBL: Z23057; CA880592.1; -
 DR EMBL: H0005729; AA005729.1; -
 DR PIR: JN0317; JN0317.
 DR HSSP: P18031; IPY.
 DR MCD: M3197805; PIPYL.
 DR InterPro: IPR000340; DS.phosphatase.
 DR InterPro: IPR000347; TYR.phosphatase.
 DR InterPro: IPR000242; TYR.proteinphosphatase.
 DR Pfam: PF00102; Y.phosphatase.1.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPC.1.
 DR PROSITE: PS00012; Y.phosphatase.1.
 DR PROSITE: PS00364; TYR.phosphatase.1.
 DR PROSITE: PS00056; TYR.phosphatase.2.
 DR PROSITE: PS00055; TYR.phosphatase_PTP.1.
 DR HydroScale: -
 FT DOMAIN 40 288 PROTEIN-TYROSINE PHOSPHATASE.
 FT AC_SITE 215 215 BY SIMILARITY.

FT CONFLICT 48 48 D -> Y (IN REF. 1).
 FT CONFLICT 104 104 S -> P (IN REF. 1).
 FT CONFLICT 173 173 H -> P (IN REF. 2).
 FT CONFLICT 266 267 GL -> HV (IN REF. 2).
 FT CONFLICT 405 405 H -> K (IN REF. 1).
 FT SEQUENCE 432 AA, 49593 MD, 484322042288048 CIRC64;
 SQ
 Query Match 31.1%; Score 79; DH 1; Length 432;
 Best Local Similarity 100.0%; Pctd. No. 7,9e-76;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 VAKLPKNNRNYRQVSPEDSRKIKLHEDNDYINSLIKMEQASYSILTPSPPTG 65
 DB 34 VAKLPKNNRNYRQVSPEDSRKIKLHEDNDYINSLIKMEQASYSILTPSPPTG 93
 OY 66 HFEWVWFGKSKGVMLNR 84
 DB 94 HFEWVWFGKSKGVMLNR 112

RESULT 3

PTN1_RAT STANDARD: PRT: 432 AA.

ID P20417;

AC 01-FEB-1991 (Ref. 17, created)

DT 01-FEB-1991 (Ref. 17, last sequence update)

DT 16-OCT-2001 (Ref. 40, last annotation update)

DE Protein-tyrosine phosphatase, non-receptor type 1 (NC 3.1.4.8)

DE (Protein-tyrosine phosphatase 1B) (PTP-1B).

GN PTPN1.

OS Patus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

CC NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Brain.

RX MEDLINE=90160354; PubMed-2154749;

RA Guan K., Han R.S., Watson S.J., Goshen R.L., Dixon J.E.

RT "Cloning and expression of a protein tyrosine phosphatase."

PL Efec. Natl. Acad. Sci. U S A. 87:1501-1505(1990).

CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein

CC tyrosine + phosphate.

CC -1- SUBCELLULAR LOCATION: ASSOCIATED TO THE ENDOPLASMIC RETICULUM VIA

CC ITS C-TERMINAL DOMAIN WITH ITS PHOSPHATASE DOMAIN ORIENTED TOWARDS

CC THE CYTOSOL.

CC -1- TISSUE SPECIFICITY: FOUND IN SEVERAL TISSUES INCLUDING CENTRAL

CC NERVOUS SYSTEM, LIVER AND KIDNEY. A HIGH LEVEL OF EXPRESSION WAS

CC FOUND IN THE HIPPOCAMPUS.

CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN

CC TYROSINE PHOSPHATASE FAMILY.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL: M33962; AAC79516.1; -

DR PIR: A34845; A34845.

DR HSSP: P18031; IPY.

DR InterPro: IPR000340; DS.phosphatase.

DR InterPro: IPR000387; TYR.phosphatase.

DR InterPro: IPR000242; TYR.proteinphosphatase.

DR Pfam: PF00102; Y.phosphatase.1.

DR PRINTS: PR00700; PRTYPHPTASE.

DR SMART: SM00194; PTPC.1.

DR PROSITE: PS00194; PTPC_DSPTC.1.

DR PROSITE: PS00193; TYR.phosphatase.1; 1.

DR PROSITE: PS00056; TYR.phosphatase.2; 1.

DR InterPro: IPR000487; TYR_phosphatase.
 DR InterPro: PS000242; Tyr_prot_phosphatase.
 DR Pfam: PF00102; Y_phosphatase_1.
 DR PRINTS: PR00700; PRTPPHPTASE.
 DR SMART: SM00194; PTPC_1.
 DR PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase; DNA-binding.
 FT DOMAIN 42 286 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 216 216 BY SIMILARITY.
 FT DNA_BIND 359 BASIC MOTIF (POTENTIAL).
 SQ SEQUENCE 363 AA; 42236 MW; 841708466D24715 CRC64.

Query Match 12.6%; Score 32; FR 1; Length 363;
 Best Local Similarity 100.0%; Freq. No. 4; 36-26;
 Matches 32; Conservative 0; Mismatches 0; Gaps 0;

DB 143 HHHYTTWPDGVESPASPLNLFKVRKESGL 174
 174 HHHYTTWPDGVESPASPLNLFKVRKESGL 205

RESULT 6
 PIN2_HUMAN STANDARD; PRT; 415 AA.
 ID PIN2_HUMAN
 AC P17706; Q96HR2;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48) (T-cell protein-tyrosine phosphatase) (TCPTP).
 GN PTNP2 OR PTP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=89315776; PubMed=2546150;
 RA "Good B., Frank N., Chabannon H., Walsh K., Fischer V.H., Krebs V.G.;
 RT "cDNA isolated from a human T-cell library encodes a member of the
 RT protein-tyrosine-phosphatase family";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5257-5261(1989)
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92115688; PubMed=1731319;
 RA "Moshiger B. Jr., Tillmann H., Westphal H., Tremblay M.L.;
 RT "Cloning and characterization of a mouse cDNA encoding a cytoplasmic
 RT protein-tyrosine phosphatase";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:499-503(1992)
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PTPB).
 RC TISSUE=Eye;
 RA Strausberg P.;
 RX SUBMITTER (MAY-2001) to the FMR1/GenBank/EMBL databases.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O -> protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2; ISOFORMS: PTPA AND PTPB (SHOWN HERE), ARE
 CC PROTECTED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PTPA ISOFORM IS PROBABLY THE MAJOR PTP
 CC EXPRESSED IN HUMAN TISSUES. PTPB ISOFORM WAS FOUND IN T-CELLS AND
 CC IN PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.ebi.ac.uk/Ensembl/
 CC or send an email to licences@ebi.ac.uk).

DR EMBL: M25393; AAA65997.1; -
 DR EMBL: M61478; -; NOT_ANNOTATED_CDS.
 DR EMBL: BC008244, AA08244.1, -
 DR FTR: A33899; A33899.
 DR HSSP: P18031; 1PTV.
 DR MIM: 176887; -;
 DR Trn-Proto, IPR000487, TYR_phosphatase
 DR InterPro: IPR000242; Tyr_prot_phosphatase.
 DR Pfam: PF00102; Y_phosphatase_1.
 DR PRINTS: PR00700; PRTPPHPTASE.
 DR SMART: SM00194; PTPC_1.
 DR PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase; Y-cell; Alternative splicing.
 FT DOMAIN 42 286 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 216 216 BY SIMILARITY.
 FT VARSPLIC 382 415 WYMDITKMFMSVLIWCAVGMPLFQGNL -> PRL
 FT TDT (TN ISOFORM PTPA).
 SQ SEQUENCE 415 AA; 48528 MW; 05996944F058F08 CRC64;

Query Match 12.6%; Score 32; DB 1; Length 415;
 Best Local Similarity 100.0%; Freq. No. 5; 66-26;
 Matches 32; Conservative 0; Mismatches 0; Gaps 0;

DB 143 HHHYTTWPDGVESPASPLNLFKVRKESGL 174
 174 HHHYTTWPDGVESPASPLNLFKVRKESGL 205

RESULT 7
 PIN2_MOUSE STANDARD; PRT; 382 AA.
 ID PIN2_MOUSE
 AC Q06180;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48)
 DE (protein tyrosine phosphatase PTP 2) (MPTP).
 GN PTNP2 OR PTP.
 OS Mus musculus (Mouse).
 OC Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92115688; PubMed=1731319;
 RA "Moshiger B. Jr., Tillmann H., Westphal H., Tremblay M.L.;
 RT "Cloning and characterization of a mouse cDNA encoding a cytoplasmic
 RT protein tyrosine phosphatase";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:499-503(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6N; TISSUE=Testis; and T-cell;
 RX MEDLINE=93140736; PubMed=1283199;
 RA Miyasaka H., Li S. L.;
 RT "Molecular cloning, nucleotide sequence and expression of a cDNA
 RT encoding an intracellular protein tyrosine phosphatase, PTPase-2,
 RT from mouse testis and T-cells";
 RL Mol. Cell. Biochem. 118:91-98(1992)
 CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2)O -> protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE EXAMINED TISSUES. THE HIGHEST
 CC EXPRESSION LEVELS WERE FOUND IN OVARY, TESTES, THYMUS AND
 CC KIDNEYS. ALSO PRESENT IN SPLEEN, MONOCYTES, LIVER, HEART AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.

CC -1- TISSUE SPECIFICITY: IN THE ANTERIOR-LINK AND POSTERIOR-LINK TYROS.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT MODERATE LEVELS DURING GROWTH
 CC AND DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.sib.ch/announce/>
 CC or send an email to license@isb.sib.ch).
 CC -----
 CC EMBL: 038197; AAC7041.1; -
 CC HSP: G06124; 25HP.
 CC DictyDB: D00111; P1PC1.
 CC DictyDB: P00000; P1PC2.
 CC InterPro: IPR000387; TYR_PHSPTASE.
 CC InterPro: IPR000242; TYR_prot_phphatase.
 CC Pfam: PF00102; Y_PHSPTASE_1.
 CC PRINTS: PR00700; PRTYPHPTASE.
 CC SMART: SM00194; PTPC; 1.
 CC PROSITE: PS00383; TYR_PHSPTASE_1; 1.
 CC PROSITE: PS00356; TYR_PHSPTASE_2; 1.
 CC PROSITE: PS00055; TYR_PHSPTASE_PTP; 1.
 CC Hydrolase.
 CC KM
 CC FT ACT_SITE 649 649 BY SIMILARITY.
 CC FT DOMAIN 460 716 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT DOMAIN 64 71 POLY-ASN.
 CC FT DOMAIN 109 118 POLY-ASN.
 CC FT DOMAIN 137 190 POLY-ASN.
 CC FT DOMAIN 249 257 POLY-SER.
 CC FT DOMAIN 258 265 POLY-SER.
 CC FT DOMAIN 286 289 POLY-ASN.
 CC FT DOMAIN 366 371 POLY-SER.
 CC FT DOMAIN 787 790 POLY-SER.
 CC FT DOMAIN 834 839 POLY-SER.
 CC FT DOMAIN 883 892 POLY-SER.
 CC FT DOMAIN 906 914 POLY-ASN.
 CC FT DOMAIN 943 963 POLY-ASN.
 CC FT SHOUENCE 989 AA: 109995 MW: 9371105AP80974AP CR664;
 SO
 Query Match 5.1%; Score 13; DB 1; Length 989;
 Best Local Similarity 100.0%; Pred. No. 1.8e 05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 183 VHCAGAGGSGIF 195
 DB 647 VHCAGAGGSGIF 659
 RESULT 13
 PIND_HUMAN STANDARD; PRT; 926 AA.
 AC P29074;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 4 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase MOC1) (PTPase-MOC1) (MOC).
 GN PTPN4
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCHI_TaxID:9606;
 CC 111
 RN SEQUENCE FROM N.A.
 RP MEDLINE:91288564; PubMed:1648233;
 RA Gu M., York J.D., Warshawsky I., Majerus P.W.;
 RT Identification, cloning, and expression of a cytosolic megakaryocyte
 RT protein-tyrosine-phosphatase with sequence homology to cytoskeletal

RT protein 4.1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:5867-5871 (1991).
 CC -1- FUNCTION: MAY ACT AT JUNCTIONS BETWEEN THE MEMBRANE AND THE
 CC CYTOSKELETON.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase (H2O) - protein
 CC tyrosine + phosphate.
 CC -1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.sib.ch/announce/>
 CC or send an email to license@isb.sib.ch).
 CC -----
 CC EMBL: M68941; AAA36530.1; -
 CC EIR: A41105; A41105.
 CC EIR: P18552; LYFO.
 CC MIM: 176878;
 CC InterPro: IPR000299; Rand_4.1.
 CC InterPro: IPR001478; PDZ.
 CC InterPro: IPR000387; TYR_PHSPTASE.
 CC InterPro: IPR000242; TYR_prot_phphatase.
 CC Pfam: PF00373; Band_41; 1.
 CC Pfam: PF00595; PDZ; 1.
 CC Pfam: PF00102; Y_PHSPTASE; 1.
 CC PRINTS: PR00935; HAND4.
 CC PRINTS: PR00700; PRTYPHPTASE.
 CC SMART: SM00245; B41; 1.
 CC SMART: SM00228; PDZ; 1.
 CC SMART: SM00194; PTPC; 1.
 CC PROSITE: PS00660; HAND_41_1; 1.
 CC PROSITE: PS00661; HAND_41_2; 1.
 CC PROSITE: PS00057; HAND_41_3; 1.
 CC PROSITE: PS00057; PDZ; 1.
 CC PROSITE: PS00383; TYR_PHSPTASE_1; 1.
 CC PROSITE: PS00356; TYR_PHSPTASE_2; 1.
 CC PROSITE: PS00055; TYR_PHSPTASE_PTP; 1.
 CC Structural protein; Cytoskeleton; Hydrolase.
 CC KW
 CC FT DOMAIN 84 241 HAND 4.1-LIKE.
 CC FT DOMAIN 517 589 PDZ.
 CC FT DOMAIN 677 926 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 852 852 BY SIMILARITY.
 CC SHOUENCE 926 AA: 105911 MW: 40AC6A87A675CP80 CR664;
 SO
 Query Match 4.7%; Score 12; DB 1; Length 926;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 180 PVVHCAGAGG 191
 DB 847 PVVHCAGAGG 858
 RESULT 14
 PIND_HUMAN STANDARD; PRT; 2485 AA.
 AC Q12923; Q15263; Q15264; Q15265; Q15266; Q15267;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 1E) (PTP 1E) (PTP 1E) (Protein tyrosine
 DE phosphatase PTP1E) (Fas-associated protein-tyrosine phosphatase 1)
 DE (FAP-1).
 GN PTPN13 OR PTP1E OR PTP1L OR PTP1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

107 Mammalian: Parthenocytotomus; Catarrhini; Hominoidea; Homo.
 108 New Taxid 9500.
 109 [1]
 110 SEQUENCE FROM N.A.
 111
 112 TISSUE: breast cartilage;
 113 MDL: 94450000; PubMed 8074550;
 114 Kunitz D., Almod S., Stocco K., Shen S. H.;
 115 "A novel protein tyrosine phosphatase with homology to both the
 116 cytoskeletal proteins of the band 4.1 family and junction associated
 117 transglutinin."
 118 J. Biol. Chem. 269:22820-22827 (1994).
 119 [2]
 120 SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 121 TISSUE: leukocyte;
 122 MEDLINE 94116679; PubMed 8287977;
 123 Markawa K., Imamura N., Nishimura M., Harada S.;
 124 "Molecular cloning of a novel protein tyrosine phosphatase containing
 125 a membrane binding domain and class repeats."
 126 J. Biol. Chem. 269:20020-20026 (1994).
 127 [3]
 128 SEQUENCE FROM N.A.
 129 TISSUE: fibroblast;
 130 MEDLINE 95041409; PubMed 7920060;
 131 Strauss J., Claesson-Welsh L., Heidin C. H., Gomez I. d.;
 132 "Cloning and characterization of p191, a protein tyrosine phosphatase
 133 with similarities to cytoskeletal associated proteins."
 134 J. Biol. Chem. 269:24082-24089 (1994).
 135 [4]
 136 SEQUENCE OF 1216-2400 FROM N.A.
 137 TISSUE: fibroblast;
 138 Submitted (JUN 1994) to the EMBL/Genbank/DBJ databases.
 139 [5]
 140 SEQUENCE BY NMR OF 1-61 1456.
 141 MEDLINE 20170042; PubMed 10704206;
 142 Kozlov G., Gehring K., Eick L.;
 143 "Solution structure of the 1762 domain from human phosphatase hPTP1C
 144 and its interactions with C-terminal peptides from the Ras
 145 receptor."
 146 J. Biochemistry 93:2772-2780 (2000).
 147 [6]
 148 TISSUE: HINDS TO A NEUTRAL REGULATORY DOMAIN IN FAS THAT
 149 INHIBITS FAS-INDUCED APOPTOSIS.
 150 CALYXIN ACTIVITY: protein tyrosine phosphatase + H(2)O - protein
 151 tyrosine + phosphate.
 152 I SUBCELLULAR LOCATION: cytoplasmic (by similarity);
 153 I ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here); 2 AND 3 ARE
 154 PRODUCED BY ALTERNATIVE SPLICING.
 155 I TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF
 156 THE LIVER AND SKELETAL MUSCLE. MOST ABUNDANT IN LUNG, KIDNEY AND
 157 FETAL BRAIN.
 158 I SIMILARITY: CONTAINS 1 BAND 4.1 LIKE DOMAIN.
 159 I SIMILARITY: BELONGS TO THE NON RECEPTOR CLASS OF THE PROTEIN-
 160 TYROSINE PHOSPHATASE FAMILY.
 161
 162 This Swiss Prot entry is copyright. It is produced through a collaboration
 163 between the Swiss Institute of Bioinformatics and the EMBL outstation.
 164 use by non profit institutions as long as its content is in no way
 165 modified and this statement is not removed. Usage by and for commercial
 166 entities requires a license agreement (see http://www.sdb.ch.ch/procov).
 167
 168
 169 EMBL: 012120; AAC000000.1;
 170 EMBL: 021209; BAA04500.1;
 171 EMBL: 021210; BAA04700.1;
 172 EMBL: 021211; BAA04750.1;
 173 EMBL: X80289; CAA05560.1;
 174 EMBL: X79676; CAA06124.1;
 175 EMBL: 010717; MAF 000;
 176 MIM: 600267;
 177 InterPro: IPR000700; Band 4.1.
 178 InterPro: IPR001476; 057.

DR InterPro: IPR000387; TYR phosphatase.
 DR InterPro: IPR000242; TYR_Prot_phphatase.
 DR Pfam: PF00374; Band_4.1; 1.
 DR Pfam: PF00595; PDZ; 5.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00935; Band4.1.
 DR PRINTS: PR00700; PRYDPHTASE.
 DR SMART: SM00295; H41; 1.
 DR SMART: SM00228; PDZ; 5.
 DR SMART: SM00194; PTPc; 1.
 DR PROSITE: PS00660; BAND_4.1; FALSE NEG.
 DR PROSITE: PS00661; BAND_4.1_2; FALSE NEG.
 DR PROSITE: PS00657; BAND_4.1_3; 1.
 DR PROSITE: PS00306; PDZ; 5.
 DR PROSITE: PS00383; TYR PHOSPHATASE; 1; FALSE NEG.
 DR PROSITE: PS00656; TYR_PHOSPHATASE; 2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 DR Structural proteins: cytoskeleton; Hydrolase; Repeat; 3D-structure;
 KW Alternative splicing; Coiled coil.
 FT DOMAIN 56
 FT DOMAIN 585-879
 FT DOMAIN 2227-2485
 FT DOMAIN 379-399
 FT DOMAIN 469-504
 FT DOMAIN 1775-1804
 FT DOMAIN 2057-2085
 FT DOMAIN 1093-1178
 FT DOMAIN 1368-1452
 FT DOMAIN 1501-1586
 FT DOMAIN 1788-1868
 FT DOMAIN 1882-1965
 FT DOMAIN 1742-1749
 FT ACT_SITE 2408-2408
 FT VARSPIC 884-1074
 FT VARSPIC 1056-1074
 FT CONFLICT 1134-1135
 FT CONFLICT 1216-1229
 FT CONFLICT 1238-1239
 FT CONFLICT 1457-1457
 FT CONFLICT 1462-1463
 FT CONFLICT 1483-1483
 FT CONFLICT 1538-1538
 FT CONFLICT 1649-1649
 FT CONFLICT 1698-1714
 FT CONFLICT 1797-1797
 FT CONFLICT 1856-1857
 FT CONFLICT 2059-2069
 FT CONFLICT 2206-2210
 FT SEQUENCE 2485 AA; 276903 MW; 801B31973660620 CIR64;
 Query Match 4.38; Score 11; DR 1; Length 2485;
 Post Local Similarity 100.0%; Proc. No. 0 0054;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 184 HCSAIGRSST 194
 DB 2407 HCSAIGRSST 2417
 RESULT 15
 ID PTN7_RAT STANDARD; PRT; 359 AA.
 AC 149445;
 DT 01-FEB-1996 (Ref. 33, Created)
 DT 01-FEB-1996 (Ref. 33, Last sequence update)
 DT 16-OCT-2001 (Ref. 40, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 7 (P⁺ 4.1.4b)
 DE (Protein-tyrosine phosphatase L⁺-PTP) (hematopoietic protein tyrosine
 DE phosphatase) (HPTP).
 DE PRTN7.


```

08 Rattus norvegicus (Rat).
09 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
00 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
01 NCHI_taxid=10116;
02 [1]
03
04 SEQUENCE FROM N.A.
05 MEDLINE=9539499; PubMed=755170;
06 Swales M., Berenstein E.H., Swalm W.D., Siraganian R.P.;
07 "Aggregation of IgE receptors in rat basophilic leukemia 2H3 cells
08 induces tyrosine phosphorylation of the cytosolic protein-tyrosine
09 phosphatase Hcyp7."
10 J. Biol. Chem. 270:21902-21906(1995).
11
12 -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF T AND B LYMPHOCYTE
13 DEVELOPMENT AND SIGNAL TRANSDUCTION (BY SIMILARITY).
14 -1- CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2)O = protein
15 tyrosine + phosphate.
16 -1- SUBCELLULAR LOCATION: cytoplasmic (by similarity)
17 -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
18 TYROSINE PHOSPHATASE FAMILY.
19
20 -----
21 This SWISS-PROT entry is copyright. It is produced through a collaboration
22 between the Swiss Institute of Bioinformatics and the EMBL collaboration -
23 the European Bioinformatics Institute. There are no restrictions on its
24 use by non-profit institutions as long as its content is in no way
25 modified and this statement is not removed. Usage by and for commercial
26 entities requires a license agreement (see http://www.isb-sib.ch/announce/
27 or send an email to license@sib-sib.ch).
28 -----
29 EMBL: U28456; AAA84443.1;
30
31 DR HSPP: P18031; 182H.
32 DR InterPro: IPR000187; TYR_phosphatase.
33 DR InterPro: IPR00242; TYR_prol_phphatase.
34 DR Pfam: P400102; Y_phosphatase; 1.
35 DR PRINTS: PR00700; PRTYPHPTASE.
36 DR SMART: SM00194; PTPc; 1.
37 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
38 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
39 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
40
41 KW Hydrolyase.
42
43 FT DOMAIN 119 342 PROTEIN TYROSINE PHOSPHATASE.
44 FT ACT_SITE 290 290 BY SIMILARITY.
45
46 SQ SEQUENCE 359 AA: 40314 MW: 5898196DB633677 CRC64:

```

```

Query Match 3.98; Score 10; DB 1; Length 359;
Host Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 182 VVHCSAGIGR 191
DB 287 VVHCSAGIGR 296

```

Search completed: June 18, 2002, 15:02:10
Job time: 115 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 15:00:15 Search time 26.52 seconds
(without alignments)
1656.890 Million cell updates/sec

Title: US-09-788-626-2

Perfect score: 254

Sequence: 1 DPCPRVAKIIPKNNNNRYDVSPPDHSIKIHKQKINQYINASIIKMHKAGKSYIIITQGITL 254

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Word size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLAE:*
9: SP_PLANT:*
10: SP_PROTOZOA:*
11: SP_VIRUS:*
12: SP_VIRUS:*
13: SP_VIRUS:*
14: SP_VIRUS:*
15: SP_VIRUS:*
16: SP_VIRUS:*
17: SP_ARCHAEA:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	50.0	414	4	Q9NQ04
2	54	21.3	62	13	Q96350
3	43	16.9	272	11	Q99JST
4	38	15.0	92	13	Q9YHE3
5	38	15.0	433	13	Q9P191
6	32	12.6	91	13	Q9YHE1
7	32	12.6	353	4	Q96A05
8	32	12.6	387	4	Q96HR2
9	30	11.8	87	13	Q9PSC7
10	30	11.8	322	13	Q91B44
11	30	11.8	406	11	Q922E7
12	16	6.3	379	13	Q9NKZ8
13	16	6.3	548	5	Q9W031
14	14	5.5	91	13	Q9YHE2
15	14	5.5	331	5	Q9N109
16	13	5.1	274	11	Q9W008

17	13	5.1	369	11	Q63419
18	13	5.1	412	4	Q9NFK5
19	13	5.1	412	11	Q9Q0H9
20	13	5.1	412	11	Q62695
21	13	5.1	451	4	Q00342
22	13	5.1	535	11	Q08617
23	13	5.1	593	13	Q90687
24	13	5.1	595	13	Q92124
25	13	5.1	597	11	Q64509
26	13	5.1	656	11	Q62132
27	13	5.1	657	4	Q15256
28	12	4.7	121	13	Q90951
29	12	4.7	121	4	Q909A7
30	12	4.7	121	13	Q91870
31	11	4.3	2460	11	Q64512
32	11	4.3	2484	6	Q28906
33	10	3.9	164	11	Q63848
34	10	3.9	225	13	Q9N101
35	10	3.9	229	5	Q9Y1W9
36	10	3.9	241	13	Q9N103
37	10	3.9	253	13	Q9N100
38	10	3.9	275	5	Q9SL10
39	10	3.9	342	10	Q82710
40	10	3.9	338	10	Q82687
41	10	3.9	342	13	Q91895
42	10	3.9	344	5	Q44901
43	10	3.9	346	5	Q966M2
44	10	3.9	352	5	Q9BL74
45	10	3.9	352	5	Q9XV04

ALIGNMENTS

RESULT 1
Q9NQ04 PRELIMINARY; PRT: 414 AA.
ID Q9NQ04;
AC Q9NQ04;
DT 01-OCT-2000 (TREMBLrel, 15, created)
DT 01-OCT-2000 (TREMBLrel, 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel, 19, last annotation update)
DE D530115.1 (PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 (EC 3.1.3.48)) (FRAGMENT).
GN PTPN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Placentalia; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wall M.;
PL S:predicted (MAP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL133230; CAC00618.1; -.
DR HSSP: P18031; 1ppp.
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR000387; Tyr_Prot_PTPase.
DR InterPro: IPR00242; Tyr_Prot_PTPase.
DR PRINTS: PR00700; PTP_PTPase.
DR SMART: SM00194; PTPc; 1.
DR SMART: SM00112; PTPc; 1.
DR PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00505; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00505; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Receptor.
FT MISC_FEATURE 1
FT MISC_FEATURE 1
SQ SQQHQHCF 414 AA; 47464 MW; 323AACAA368A4556 CMC64;

Query Match 50.0%; Score 127; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 4; 8e-125;
Matches 127; Conservative 0; Mismatches 0; Indels 0;
GX 1 DPCPRVAKIIPKNNNNRYDVSPPDHSIKIHKQKINQYINASIIKMHKAGKSYIIITQGITL 60


```

000 CYP11A1: Cytochrome P-450 11A1, Danio.
001 NCBI_TaxID=7955;
002
003
004
005
006
007
008
009
010
011
012
013
014
015
016
017
018
019
020
021
022
023
024
025
026
027
028
029
030
031
032
033
034
035
036
037
038
039
040
041
042
043
044
045
046
047
048
049
050
051
052
053
054
055
056
057
058
059
060
061
062
063
064
065
066
067
068
069
070
071
072
073
074
075
076
077
078
079
080
081
082
083
084
085
086
087
088
089
090
091
092
093
094
095
096
097
098
099
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204
2205
2206
2207
2208
2209
2210
2211
2212
2213
2214
2215
2216
2217
2218
2219
2220
2221
2222
2223
2224
2225
2226
2227
2228
2229
2230
2231
2232
2233
2234
2235
2236
2237
2238
2239
2240
2241
2242
2243
2244
2245
2246
2247
2248
2249
2250
2251
2252
2253
2254
2255
2256
2257
2258
2259
2260
2261
2262
2263
2264
2265
2266
2267
2268
2269
2270
2271
2272
2273
2274
2275
2276
2277
2278
2279
2280
2281
2282
2283
2284
2285
2286
2287
2288
2289
2290
2291
2292
2293
2294
2295
2296
2297
2298
2299
2300
2301
2302
2303
2304
2305
2306
2307
2308
2309
2310
2311
2312
2313
2314
2315
2316
2317
2318
2319
2320
2321
2322
2323
2324
2325
2326
2327
2328
2329
2330
2331
2332
2333
2334
2335
2336
2337
2338
2339
2340
2341
2342
2343
2344
2345
2346
2347
2348
2349
2350
2351
2352
2353
2354
2355
2356
2357
2358
2359
2360
2361
2362
2363
2364
2365
2366
2367
2368
2369
2370
2371
2372
2373
2374
2375
2376
2377
2378
2379
2380
2381
2382
2383
2384
2385
2386
2387
2388
2389
2390
2391
2392
2393
2394
2395
2396
2397
2398
2399
2400
2401
2402
2403
2404
2405
2406
2407
2408
2409
2410
2411
2412
2413
2414
2415
2416
2417
2418
2419
2420
2421
2422
2423
2424
2425
2426
2427
2428
2429
2430
2431
2432
2433
2434
2435
2436
2437
2438
2439
2440
2441
2442
2443
2444
2445
2446
2447
2448
2449
2450
2451
2452
2453
2454
2455
2456
2457
2458
2459
2460
2461
2462
2463
2464
2465
2466
2467
2468
2469
2470
2471
2472
2473
2474
2475
2476
2477
2478
2479
2480
2481
2482
2483
2484
2485
2486
2487
2488
2489
2490
2491
2492
2493
2494
2495
2496
2497
2498
2499
2500
2501
2502
2503
2504
2505
2506
2507
2508
2509
2510
2511
2512
2513
2514
2515
2516
2517
2518
2519
2520
2521
2522
2523
2524
2525
2526
2527
2528
2529
2530
2531
2532
2533
2534
2535
2536
2537
2538
2539
2540
2541
2542
2543
2544
2545
2546
2547
2548
2549
2550
2551
2552
2553
2554
2555
2556
2557
2558
2559
2560
2561
2562
2563
2564
2565
2566
2567
2568
2569
2570
2571
2572
2573
2574
2575
2576
2577
2578
2579
2580
2581
2582
2583
2584
2585
2586
2587
2588
2589
2590
2591
2592
2593
2594
2595
2596
2597
2598
2599
2600
2601
2602
2603
2604
2605
2606
2607
2608
2609
2610
2611
2612
2613
2614
2615
2616
2617
2618
2619
2620
2621
2622
2623
2624
2625
2626
2627
2628
2629
2630
2631
2632
2633
2634
2635
2636

```


R1 phosphatase sub families.
 R1 Submittred (Oct 1998) to the EMBL/GenBank/DBJ databases.
 R1 EMBL: AF097482; AF097483,1;
 R1 HSSP: P18041; 1PTV
 R1 InterPro: IPR002442; Tyr prot phosphatase.
 R1 PRINTS: PR00700; PR106941ASH.
 R1 PROSITE: PS50055; TYR PHOSPHATASE_PP3_1.
 R1 Hydrolyase.
 R1 NON TER 1 1
 R1 NON TER 91 91
 R1 SEQUENCE 91 AA: 10444 MW: 84286763.486741 CRC64:

Query Match 5.9% Score 14; DB 14; Length 91;
 Local Local Similarity 100.0%; Pred. No. 1,1e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 149 WDPGWYFESHASL 162
 Q6 WDPGWYFESHASL 69
 Q6 WDPGWYFESHASL 69

RESULT 15
 Q9N109

ID Q9N109 PRELIMINARY DEF: 441 AA.

DT 01 OCT 2000 (TEMMLE01: 15; Created)

DT 01 OCT 2000 (TEMMLE01: 15; Last sequence update)

DT 01 DEC 2001 (TEMMLE01: 15; Last annotation update)

DE AMPURIN PROTEIN (PRACMIN).

FN AMPURIN.

OS Branchiostoma belcheri (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

SC Branchiostoma.

NX NCBI TaxID 7741;

RN 113;

RP SEQUENCE FROM N.A.

RX MEDLINE 20219425; PubMed 10754074;

RA Yano Koyubari K.; Suga H.; Katoh K.; Miyata T.;

RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:

R1 divergence of tissue specific isoform genes in the early evolution of

R1 vertebrates."

R1 J. Mol. Evol. 50: 402-411 (2000).

R1 EMBL: AM035646; MAA95175,17;

R1 HSSP: P18041; 2HNO.

R1 InterPro: IPR000487; Tyr phosphatase.

R1 InterPro: IPR002442; Tyr prot phosphatase.

R1 PRINTS: PR00700; PR106941ASH.

R1 SMART: SM00194; PP3C_1.

R1 PROSITE: PS00483; TYR PHOSPHATASE_1; 1.

R1 PROSITE: PS50056; TYR PHOSPHATASE_2; 1.

R1 PROSITE: PS50055; TYR PHOSPHATASE_PP3_1.

R1 Hydrolyase.

R1 NON TER 1 1

R1 NON TER 91 91

R1 SEQUENCE 91 AA: 98440 MW: 4148736709459 CRC64:

Query Match 5.9% Score 14; DB 5; Length 431;

Local Local Similarity 100.0%; Pred. No. 8,5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 249 WDPGWYFESHASL 248

Q6 WDPGWYFESHASL 69

Q6 WDPGWYFESHASL 69

Q6 WDPGWYFESHASL 69

Q6 WDPGWYFESHASL 69